WEST

Help | Logout

Main Menu | Search Form | Posting Counts | Show S Numbers | Edit S Numbers

09/380,932

Search Results -

Terms	Documents
l4 and ligating	1

Database: US Patents Full-Text Database

Refine Search: 14 and ligating

Search History

DB Name	Query	Hit Count	Set Name
USPT	l4 and ligating	1	L5
USPT	l3 and flanking	34	L4
USPT	l2 and ((variable adj number adj tandem adj repeat) or VNTR)	37	L3
USPT	l1 and polymorphism	1014	L2
USPT	genomic and tag and fragment and oligonucleotide	3386	L1

WEST

Help | Logout

Main Menu | Search Form | Posting Counts | Show S Numbers | Edit S Numbers

Search Results -

Terms	Documents
l2 and ((variable adj number adj tandem adj repeat) or VNTR)	37

Database: US Patents Full-Text Database

Refine Search:

```
l2 and ((variable adj number adj tandem
adj repeat) or VNTR)
```

Search History

DB Name	Query	Hit Count	Set Name
USPT	l2 and ((variable adj number adj tandem adj repeat) or VNTR)	37	L3
USPT	l1 and polymorphism	1014	L2
USPT	genomic and tag and fragment and oligonucleotide	3386	L1

WEST

Help | Logout

Main Menu | Search Form | Posting Counts | Show S Numbers | Edit S Numbers

Generate Collection

Search Results - Record(s) 1 through 37 of 37 returned.

1. Document ID: US 6043031 A
Entry 1 of 37 File: USPT Mar 28, 2000

US-PAT-NO: 6043031
DOCUMENT-IDENTIFIER: US 6043031 A
TITLE: DNA diagnostics based on mass spectrometry

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Image

2. Document ID: US 6027896 A
Entry 2 of 37 File: USPT Feb 22, 2000

US-PAT-NO: 6027896
DOCUMENT-IDENTIFIER: US 6027896 A
TITLE: Methods of detecting Alzheimer's disease

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Image

3. Document ID: US 6027890 A
Entry 3 of 37 File: USPT Feb 22, 2000

US-PAT-NO: 6027890
DOCUMENT-IDENTIFIER: US 6027890 A
TITLE: Methods and compositions for enhancing sensitivity in the analysis of biological-based assays

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Image

4. Document ID: US 6013444 A
Entry 4 of 37 File: USPT Jan 11, 2000

US-PAT-NO: 6013444
DOCUMENT-IDENTIFIER: US 6013444 A
TITLE: DNA bracketing locus compatible standards for electrophoresis

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Image

5. Document ID: US 5981185 A
Entry 5 of 37 File: USPT Nov 9, 1999

US-PAT-NO: 5981185
DOCUMENT-IDENTIFIER: US 5981185 A
TITLE: Oligonucleotide repeat arrays

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Image

☐ 6. Document ID: US 5952190 A
Entry 6 of 37 File: USPT Sep 14, 1999

US-PAT-NO: 5952190
DOCUMENT-IDENTIFIER: US 5952190 A
TITLE: cDNA for fanconi anemia complementation group A

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Image

☐ 7. Document ID: US 5935787 A
Entry 7 of 37 File: USPT Aug 10, 1999

US-PAT-NO: 5935787
DOCUMENT-IDENTIFIER: US 5935787 A
TITLE: Detection of hypermutable nucleic acid sequence in tissue

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Image

☐ 8. Document ID: US 5919626 A
Entry 8 of 37 File: USPT Jul 6, 1999

US-PAT-NO: 5919626
DOCUMENT-IDENTIFIER: US 5919626 A
TITLE: Attachment of unmodified nucleic acids to silanized solid phase surfaces

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Image

☐ 9. Document ID: US 5879884 A
Entry 9 of 37 File: USPT Mar 9, 1999

US-PAT-NO: 5879884
DOCUMENT-IDENTIFIER: US 5879884 A
TITLE: Diagnosis of depression by linkage of a polymorphic marker to a segment of chromosome 19P13 bordered by D19S247 and D19S394

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Image

☐ 10. Document ID: US 5861283 A
Entry 10 of 37 File: USPT Jan 19, 1999

US-PAT-NO: 5861283
DOCUMENT-IDENTIFIER: US 5861283 A
TITLE: DNA encoding a limbic system-associated membrane protein

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Image

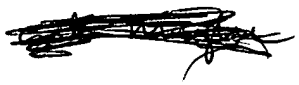
☐ 11. Document ID: US 5853988 A
Entry 11 of 37 File: USPT Dec 29, 1998

US-PAT-NO: 5853988
DOCUMENT-IDENTIFIER: US 5853988 A
TITLE: Diagnosis of retinoblastoma

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Image

☐ 12. Document ID: US 5853989 A
Entry 12 of 37 File: USPT Dec 29, 1998

US-PAT-NO: 5853989
DOCUMENT-IDENTIFIER: US 5853989 A
TITLE: Method of characterisation of genomic DNA



Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Image

☐ 13. Document ID: US 5851769 A
Entry 13 of 37 File: USPT Dec 22, 1998

US-PAT-NO: 5851769
DOCUMENT-IDENTIFIER: US 5851769 A
TITLE: Quantitative DNA fiber mapping

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Image

☐ 14. Document ID: US 5849544 A
Entry 14 of 37 File: USPT Dec 15, 1998

US-PAT-NO: 5849544
DOCUMENT-IDENTIFIER: US 5849544 A
TITLE: Amplification and detection process

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Image

☐ 15. Document ID: US 5843660 A
Entry 15 of 37 File: USPT Dec 1, 1998

US-PAT-NO: 5843660
DOCUMENT-IDENTIFIER: US 5843660 A
TITLE: Multiplex amplification of short tandem repeat loci

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Image

☐ 16. Document ID: US 5843669 A
Entry 16 of 37 File: USPT Dec 1, 1998

US-PAT-NO: 5843669
DOCUMENT-IDENTIFIER: US 5843669 A
TITLE: Cleavage of nucleic acid acid using thermostable methoanococcus jannaschii FEN-1 endonucleases

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Image

☐ 17. Document ID: US 5834183 A
Entry 17 of 37 File: USPT Nov 10, 1998

US-PAT-NO: 5834183
DOCUMENT-IDENTIFIER: US 5834183 A
TITLE: Gene sequence for spinocerebellar ataxia type 1 and method for diagnosis

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Image

☐ 18. Document ID: US 5811233 A
Entry 18 of 37 File: USPT Sep 22, 1998

US-PAT-NO: 5811233
DOCUMENT-IDENTIFIER: US 5811233 A
TITLE: Compositions and uses thereof in the diagnosis of psoriasis

many hits

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Image

☐ 19. Document ID: US 5811235 A
Entry 19 of 37 File: USPT Sep 22, 1998

US-PAT-NO: 5811235
DOCUMENT-IDENTIFIER: US 5811235 A
TITLE: Method of characterisation

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Image

☐ 20. Document ID: US 5795976 A
Entry 20 of 37 File: USPT Aug 18, 1998

US-PAT-NO: 5795976
DOCUMENT-IDENTIFIER: US 5795976 A
TITLE: Detection of nucleic acid heteroduplex molecules by denaturing high-performance liquid chromatography and methods for comparative sequencing

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Image

☐ 21. Document ID: US 5783666 A
Entry 21 of 37 File: USPT Jul 21, 1998

US-PAT-NO: 5783666
DOCUMENT-IDENTIFIER: US 5783666 A
TITLE: APC (adenomatous polyosis coli) protein

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Image

☐ 22. Document ID: US 5783406 A
Entry 22 of 37 File: USPT Jul 21, 1998

US-PAT-NO: 5783406
DOCUMENT-IDENTIFIER: US 5783406 A
TITLE: Allelic ladders for short tandem repeat loci

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Image

☐ 23. Document ID: US 5756696 A
Entry 23 of 37 File: USPT May 26, 1998

US-PAT-NO: 5756696
DOCUMENT-IDENTIFIER: US 5756696 A
TITLE: Compositions for chromosome-specific staining

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Image

☐ 24. Document ID: US 5753441 A
Entry 24 of 37 File: USPT May 19, 1998

US-PAT-NO: 5753441
DOCUMENT-IDENTIFIER: US 5753441 A
TITLE: 170-linked breast and ovarian cancer susceptibility gene

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Image

☐ 25. Document ID: US 5747282 A
Entry 25 of 37 File: USPT May 5, 1998

US-PAT-NO: 5747282
DOCUMENT-IDENTIFIER: US 5747282 A
TITLE: 17Q-linked breast and ovarian cancer susceptibility gene

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Image

☐ 26. Document ID: US 5720928 A
Entry 26 of 37 File: USPT Feb 24, 1998

US-PAT-NO: 5720928
DOCUMENT-IDENTIFIER: US 5720928 A
TITLE: Image processing and analysis of individual nucleic acid molecules

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Image

☐ 27. Document ID: US 5709999 A
Entry 27 of 37 File: USPT Jan 20, 1998

US-PAT-NO: 5709999
DOCUMENT-IDENTIFIER: US 5709999 A
TITLE: Linked breast and ovarian cancer susceptibility gene

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Image

☐ 28. Document ID: US 5691454 A
Entry 28 of 37 File: USPT Nov 25, 1997

US-PAT-NO: 5691454
DOCUMENT-IDENTIFIER: US 5691454 A
TITLE: APC antibodies

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Image

☐ 29. Document ID: US 5681942 A
Entry 29 of 37 File: USPT Oct 28, 1997

US-PAT-NO: 5681942
DOCUMENT-IDENTIFIER: US 5681942 A
TITLE: Fanconi Anemia Type C gene

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Image

☐ 30. Document ID: US 5674686 A
Entry 30 of 37 File: USPT Oct 7, 1997

US-PAT-NO: 5674686
DOCUMENT-IDENTIFIER: US 5674686 A
TITLE: Allelic ladders for short tandem repeat loci

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Image

☐ 31. Document ID: US 5648212 A
Entry 31 of 37 File: USPT Jul 15, 1997

US-PAT-NO: 5648212
DOCUMENT-IDENTIFIER: US 5648212 A
TITLE: Detection of inherited and somatic mutations of APC gene in colorectal cancer of humans

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Image

☐ 32. Document ID: US 5599666 A
Entry 32 of 37 File: USPT Feb 4, 1997

US-PAT-NO: 5599666
DOCUMENT-IDENTIFIER: US 5599666 A
TITLE: Allelic ladders for short tandem repeat loci

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Image

☐ 33. Document ID: US 5449604 A
Entry 33 of 37 File: USPT Sep 12, 1995

US-PAT-NO: 5449604
DOCUMENT-IDENTIFIER: US 5449604 A
TITLE: Chromosome 14 and familial Alzheimers disease genetic markers and assays

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Image

☐ 34. Document ID: US 5411859 A
Entry 34 of 37 File: USPT May 2, 1995

US-PAT-NO: 5411859
DOCUMENT-IDENTIFIER: US 5411859 A
TITLE: Genetic identification employing DNA probes of variable number tandem repeat loci

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Image

☐ 35. Document ID: US 5364759 A

Entry 35 of 37 File: USPT Nov 15, 1994

US-PAT-NO: 5364759
DOCUMENT-IDENTIFIER: US 5364759 A
TITLE: DNA typing with short tandem repeat polymorphisms and identification of polymorphic short tandem repeats

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Image

☐ 36. Document ID: US 5352775 A

Entry 36 of 37 File: USPT Oct 4, 1994

US-PAT-NO: 5352775
DOCUMENT-IDENTIFIER: US 5352775 A
TITLE: APC gene and nucleic acid probes derived therefrom

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Image

☐ 37. Document ID: US 4963663 A

Entry 37 of 37 File: USPT Oct 16, 1990

US-PAT-NO: 4963663
DOCUMENT-IDENTIFIER: US 4963663 A
TITLE: Genetic identification employing DNA probes of variable number tandem repeat loci

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Image

Generate Collection

Terms	Documents
l2 and ((variable adj number adj tandem adj repeat) or VNTR)	37

Display 40 Documents including document number

Display Format: Change Format

Main Menu | Search Form | Posting Counts | Show S Numbers | Edit S Numbers

Help | Logout

Firth
WO 98/42867
VNTR
4/17/00

```
Logging in to Dialog

Trying 3106900061...Open

DIALOG INFORMATION SERVICES
PLEASE LOGON:
 ********
ENTER PASSWORD:
□T840LCPQ
 ********
Welcome to DIALOG

Dialog leel 00.03.02D

Lat logoff:  17apr00 15:54:21
Logon file001 17apr00 19:56:38
□dialog

File   1:ERIC  1966-2000/Feb
       (c) format only 2000 The Dialog Corporation
*File   1: File has been reloaded. See HELP NEWS 1.

      Set  Items  Description
      ---  -----  -----------
? b 410

>>>'IALOG' not recognized as set or accession number
? set hi ;set hi

       17apr00 19:56:44 User233835 Session D393.1
            $0.35    0.101 DialUnits File1
     $0.35  Estimated cost File1
     $0.05  TYMNET
     $0.40  Estimated cost this search
     $0.40  Estimated total session cost   0.101 DialUnits

File 410:Chronolog(R)  1981-2000 Mar/Apr
       (c) 2000 The Dialog Corporation plc

      Set  Items  Description
      ---  -----  -----------
?
HILIGHT set on as ''
HILIGHT set on as ''
? B 155, 5, 399, 357, 654

       17apr00 19:57:18 User233835 Session D393.2
            $0.00    0.049 DialUnits File410
     $0.00  Estimated cost File410
     $0.03  TYMNET
     $0.03  Estimated cost this search
     $0.43  Estimated total session cost   0.150 DialUnits

SYSTEM:OS  - DIALOG OneSearch
  File 155:MEDLINE(R)  1966-2000/Jun W2
         (c) format only 2000 Dialog Corporation
*File 155: MEDLINE will be reloaded. Accession numbers will change.
  File   5:Biosis Previews(R)  1969-2000/Apr W3
```

(c) 2000 BIOS[redacted]
File 399:CA SEARCH(R) 1967-2000/UD=13216
(c) 2000 American Chemical Society
*File 399: Use is subject to the terms of your user/customer agreement.
RANK charge added; see HELP RATES 399.
File 357:Derwent Biotechnology Abs 1982-2000/Apr B2
(c) 2000 Derwent Publ Ltd
File 654:US Pat.Full. 1990-2000/Apr 11
(c) format only 2000 The Dialog Corp.
*File 654: Reassignment data current through 12/06/1999 recordings.
Due to recent processing problems, the SORT command is not working.

Set	Items	Description

? e au=Firth, Greg

Ref	Items	Index-term
E1	1	AU=FIRTH, GARY B.
E2	1	AU=FIRTH, GERALD R.
E3	1	*AU=FIRTH, GREG
E4	3	AU=FIRTH, H.
E5	1	AU=FIRTH, I C
E6	1	AU=FIRTH, I. C.
E7	1	AU=FIRTH, I. M.
E8	1	AU=FIRTH, IAN
E9	1	AU=FIRTH, IAN M.
E10	1	AU=FIRTH, IAN Y.
E11	8	AU=FIRTH, J.
E12	14	AU=FIRTH, J. A.

Enter P or PAGE for more
? s e3

S1 1 AU="FIRTH, GREG"
? t s1/6/1

1/6/1 (Item 1 from file: 399)
DIALOG(R)File 399:(c) 2000 American Chemical Society. All rts. reserv.

Extraction of VNTR alleles and detection of polymorphic markers for inherited traits at multiple loci
? t s1/7/1

1/7/1 (Item 1 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)
(c) 2000 American Chemical Society. All rts. reserv.

129271497 CA: 129(21)271497x PATENT
Extraction of VNTR alleles and detection of polymorphic markers for inherited traits at multiple loci
INVENTOR(AUTHOR): Firth, Greg
LOCATION: UK,
PATENT: PCT International ; WO 9842867 A1 DATE: 19981001
APPLICATION: WO 98GB840 (19980320)
PAGES: 101 pp. CODEN: PIXXD2 LANGUAGE: English CLASS: C12Q-001/68A
DESIGNATED COUNTRIES: AL; AM; AT; AU; AZ; BA; BB; BG; BR; BY; CA; CH; CN; CU; CZ; DE; DK; EE; ES; FI; GB; GE; GH; GM; GW; HU; ID; IL; IS; JP; KE; KG; KP; KR; KZ; LC; LK; LR; LS; LT; LU; LV; MD; MG; MK; MN; MW; MX; NO; NZ; PL; PT; RO; RU; SD; SE; SG; SI; SK; SL; TJ; TM; TR; TT; UA; UG; US; UZ; VN; YU; ZW; AM; AZ; BY; KG; KZ; MD; RU; TJ; TM DESIGNATED REGIONAL: GH; GM; KE; LS ; MW; SD; SZ; UG; ZW; AT; BE; CH; DE; DK; ES; FI; FR; GB; GR; IE; IT; LU; MC; NL; PT; SE; BF; BJ; CF; CG; CI; CM; GA; GN; ML; MR; NE; SN; TD; TG

SECTION:
CA203001 Biochemical [redacted]etics
IDENTIFIERS: VNTR allele isolation TRAIT, polymorphism marker inherited trait multiple loci
DESCRIPTORS:
Oligonucleotides...
double-stranded, phosphorothioate-linked, 3'-blocked; extn. of VNTR alleles and detection of polymorphic markers for inherited traits at multiple loci
Alleles... Genetic markers... Nucleic acid hybridization...
Polymorphism(genetic)... Primers(nucleic acid)... VNTR(DNA)...
extn. of VNTR alleles and detection of polymorphic markers for inherited traits at multiple loci
? e au=Firth, G

Ref	Items	Index-term
E1	4	AU=FIRTH, FRANCIS G.
E2	1	AU=FIRTH, FRANK E.
E3	0	*AU=FIRTH, G
E4	5	AU=FIRTH, G.
E5	2	AU=FIRTH, G. B.
E6	4	AU=FIRTH, GARY
E7	1	AU=FIRTH, GARY B
E8	1	AU=FIRTH, GARY B.
E9	1	AU=FIRTH, GERALD R.
E10	1	AU=FIRTH, GREG
E11	3	AU=FIRTH, H.
E12	1	AU=FIRTH, I C

Enter P or PAGE for more
? s e4

S2 5 AU="FIRTH, G."
? t s2/6/1-5

2/6/1 (Item 1 from file: 399)
DIALOG(R)File 399:(c) 2000 American Chemical Society. All rts. reserv.

The analysis of aqueous humor constituents using capillary zone electrophoresis

2/6/2 (Item 2 from file: 399)
DIALOG(R)File 399:(c) 2000 American Chemical Society. All rts. reserv.

Studies on the intracerebral injection of vincristine free and entrapped within liposomes in the rat

2/6/3 (Item 3 from file: 399)
DIALOG(R)File 399:(c) 2000 American Chemical Society. All rts. reserv.

Studies on the intracerebral injection of bleomycin free and entrapped within liposomes in the rat

2/6/4 (Item 4 from file: 399)
DIALOG(R)File 399:(c) 2000 American Chemical Society. All rts. reserv.

Studies on the use of antimitotic drugs entrapped within liposomes and of their action on a human glioma cell line

2/6/5 (Item 5 from file: 399)
DIALOG(R)File 399:(c) 2000 American Chemical Society. rts. reserv.

Value of measuring serum angiotensin I converting enzyme and serum lysozyme in the management of sarcoidosis

? s variable(w)number(w)tandem(w)repeat

```
          395106  VARIABLE
         1716121  NUMBER
           54940  TANDEM
          135318  REPEAT
      S3     461  VARIABLE(W)NUMBER(W)TANDEM(W)REPEAT
```

? s variable(w)number(w)tandem(w)repeat(w)allele

```
          395106  VARIABLE
         1716121  NUMBER
           54940  TANDEM
          135318  REPEAT
           78041  ALLELE
      S4       2  VARIABLE(W)NUMBER(W)TANDEM(W)REPEAT(W)ALLELE
```

? rd

>>>Duplicate detection is not supported for File 654.

>>>Records from unsupported files will be retained in the RD set.
...completed examining records

```
      S5       2  RD (unique items)
```

? t s5/6/1-2

5/6/1 (Item 1 from file: 5)
11889421 BIOSIS NO.: 199900135530
Association of ulcerative colitis with rare VNTR alleles of the human intestinal mucin gene, MUC3.
1999

5/6/2 (Item 1 from file: 357)
0230736 DBA Accession No.: 99-00837
Use of **variable number tandem repeat allele** and their flanking region - for genetic fingerprinting or other method of genotyping individual 1998

? t s5/7/1-2

5/7/1 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2000 BIOSIS. All rts. reserv.

11889421 BIOSIS NO.: 199900135530
Association of ulcerative colitis with rare VNTR alleles of the human intestinal mucin gene, MUC3.
AUTHOR: Kyo Kennoki; Parkes Miles; Takei Yoshiki; Nishimori Hiroyuki; Vyas Paulomi; Satsangi Jack; Simmons Jon; Nagawa Hirokazu; Baba Shozo; Jewell Derek; Muto Tetsuichiro; Lathrop G Mark; Nakamura Yusuke(a)
AUTHOR ADDRESS: (a)Lab. Molecular Med., Human Genome Center, Inst. Medical Science, Univ. Tokyo, 4-6-1, Shirokaneda**Japan
JOURNAL: Human Molecular Genetics 8 (2):p307-311 Feb., 1999
ISSN: 0964-6906
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Ulcerative colitis (UC), a common form of inflammatory bowel disease, is a multifactorial disorder with significant genetic influence.

Recently, evidence of linkage on chromosome 7q near the intestinal mucin gene MUC3 was reported by an affected sib-pair analysis. Previous reports indicate a possible mucin abnormality in UC patients, but whether genetic differences in a specific mucin gene are associated with UC is unknown. Here we analysed polymorphisms of variable number of tandem repeats (VNTRs) within this gene using DNAs obtained from 243 Japanese (75 patients with UC and 168 controls), and to confirm the result we undertook a two-stage examination using 328 Caucasian samples (72 and 85 with UC in the first and second stages, respectively, and 171 controls). When the frequency of patients carrying one or two rare VNTR alleles was compared with that of controls, a significant increase was found first in Japanese patients (odds ratio 2.72, 95% CI 1.17-6.32, P = 0.0308). In Caucasians, the odds ratio was 2.80 (95% CI 1.36-5.75, P= 0.0079) in the first stage, 2.43 (95% CI 1.20-4.92, P = 0.0196) in the second stage and 2.60 (95% CI 1.41-4.80, P= 0.0024) in total. The overall odds ratio was 2.64 (95% CI 1.60-4-33, P = 0.0001). This result suggests that rare alleles of the MUC3 gene may confer genetic predisposition to UC.

5/7/2 (Item 1 from file: 357)
DIALOG(R)File 357:Derwent Biotechnology Abs

0230736 DBA Accession No.: 99-00837 PATENT
Use of **variable number tandem repeat allele** and their flanking region - for genetic fingerprinting or other method of genotyping individual
AUTHOR: Firth G
CORPORATE SOURCE: Hitchin, UK.
PATENT ASSIGNEE: Firth G 1998
PATENT NUMBER: WO 9842867 PATENT DATE: 981001 WPI ACCESSION NO.: 98-609895 (9851)
PRIORITY APPLIC. NO.: EP 97301917 APPLIC. DATE: 970321
NATIONAL APPLIC. NO.: WO 98GB840 APPLIC. DATE: 980320
LANGUAGE: English
ABSTRACT: A method for the extraction of variable number tandem repeat polymorphism (VNTR) alleles is claimed and comprises making a mixture of VNTR alleles and their flanking regions from genomic DNA by: ligating an adaptor to genomic DNA fragments so that the 3' end of the adaptor-terminated fragment is blocked to prevent chain extension, and using these with adaptor-DNA primers and VNTR sense and antisense DNA to generate 3'- and 5'-flanking VNTR amplimers; and using the amplimers as DNA primers to extend on genomic DNA as the template and create the desired mixture of VNTR alleles and their flanking regions. Also claimed are: a method for treating a mixture of polymorphic alleles representative of a desired trait, by separating and re-annealing the DNA strands and discarding mismatches; and a method for identifying an allele-linked to a trait by hybridizing a polymorphic allele representative of the trait with a mixture of non-trait alleles and selecting matches or mismatches to isolate the polymorphic trait-linked allele. The alleles generated can be used for genetic fingerprinting or obtaining selectable markers which segregate with specific traits. (101pp)
? s s1 and polymorphism

```
             1  S1
        160329  POLYMORPHISM
     S6      1  S1 AND POLYMORPHISM
```

? t s6/6

6/6/1 (Item 1 from file: 399)
DIALOG(R)File 399:

Extraction of VNTR alleles and detection of polymorphic markers for

inherited traits at multiple loci
? t s6/7

6/7/1 (Item 1 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)

129271497 CA: 129(21)271497x PATENT
Extraction of VNTR alleles and detection of polymorphic markers for inherited traits at multiple loci
INVENTOR(AUTHOR): Firth, Greg
LOCATION: UK,
PATENT: PCT International ; WO 9842867 A1 DATE: 19981001
APPLICATION: WO 98GB840 (19980320)
PAGES: 101 pp. CODEN: PIXXD2 LANGUAGE: English CLASS: C12Q-001/68A
DESIGNATED COUNTRIES: AL; AM; AT; AU; AZ; BA; BB; BG; BR; BY; CA; CH; CN; CU; CZ; DE; DK; EE; ES; FI; GB; GE; GH; GM; GW; HU; ID; IL; IS; JP; KE; KG; KP; KR; KZ; LC; LK; LR; LS; LT; LU; LV; MD; MG; MK; MN; MW; MX; NO; NZ; PL; PT; RO; RU; SD; SE; SG; SI; SK; SL; TJ; TM; TR; TT; UA; UG; US; UZ; VN; YU; ZW; AM; AZ; BY; KG; KZ; MD; RU; TJ; TM DESIGNATED REGIONAL: GH; GM; KE; LS; MW; SD; SZ; UG; ZW; AT; BE; CH; DE; DK; ES; FI; FR; GB; GR; IE; IT; LU; MC; NL; PT; SE; BF; BJ; CF; CG; CI; CM; GA; GN; ML; MR; NE; SN; TD; TG
SECTION:
CA203001 Biochemical Genetics
IDENTIFIERS: VNTR allele isolation TRAIT, polymorphism marker inherited trait multiple loci
DESCRIPTORS:
Oligonucleotides...
double-stranded, phosphorothioate-linked, 3'-blocked; extn. of VNTR alleles and detection of polymorphic markers for inherited traits at multiple loci
Alleles... Genetic markers... Nucleic acid hybridization...
Polymorphism(genetic)... Primers(nucleic acid)... VNTR(DNA)...
extn. of VNTR alleles and detection of polymorphic markers for inherited traits at multiple loci
? DS

Set	Items	Description
S1	1	AU="FIRTH, GREG"
S2	5	AU="FIRTH, G."
S3	461	VARIABLE(W)NUMBER(W)TANDEM(W)REPEAT
S4	2	VARIABLE(W)NUMBER(W)TANDEM(W)REPEAT(W)ALLELE
S5	2	RD (unique items)
S6	1	S1 AND POLYMORPHISM

? s s3 and polymorphism

461 S3
160329 POLYMORPHISM
S7 252 S3 AND POLYMORPHISM
? s s7 and flanking

252 S7
50563 FLANKING
S8 34 S7 AND FLANKING
? rd

>>>Duplicate detection is not supported for File 654.

>>>Records from unsupported files will be retained in the RD set.
...completed examining records
S9 31 RD (unique items)
? t s9/6/1-31

9/6/1 (Item 1 from file: 155)
10019865 99303259
Characterization of a **variable number tandem repeat** region in the thiopurine S-methyltransferase gene promoter.
Apr 1999

9/6/2 (Item 2 from file: 155)
09296867 97449816
Products of partial digestion with Hae III. Part 1. Characterization, casework experience and confirmation of the theory of three-, four- and five-banded RFLP pattern origins using partial digestion.
Sep 1997

9/6/3 (Item 3 from file: 155)
06500589 91033793
Rapid diagnosis of Miller-Dieker syndrome and isolated lissencephaly sequence by the polymerase chain reaction.
Oct 1990

9/6/4 (Item 1 from file: 5)
12198641 BIOSIS NO.: 199900493490
Characterization of a **variable number tandem repeat** region in the thiopurine S-methyltransferase gene promoter.
1999

9/6/5 (Item 2 from file: 5)
08726704 BIOSIS NO.: 199395016055
Characterization of a porcine **variable number tandem repeat** sequence specific for the glucosephosphate isomerase locus.
1992

9/6/6 (Item 3 from file: 5)
07331090 BIOSIS NO.: 000090110992
RAPID DETECTION OF HYPERVARIABLE REGIONS BY THE POLYMERASE CHAIN REACTION TECHNIQUE
1990

9/6/7 (Item 1 from file: 399)

DNA sequences from specific human genomic loci useful for identification of individuals

9/6/8 (Item 1 from file: 357)
0230736 DBA Accession No.: 99-00837
Use of **variable number tandem repeat** allele and their **flanking** region - for genetic fingerprinting or other method of genotyping individual 1998

9/6/9 (Item 1 from file: 654)
03067992
DNA BRACKETING LOCUS COMPATIBLE STANDARDS FOR ELECTROPHORESIS
FULL TEXT: 1867 lines

9/6/10 (Item 2 from file: 654)

03028379
COMPARATIVE GENOMIC HY[redacted]DIZATION (CGH)
FULL TEXT: 3594 lines

9/6/11 (Item 3 from file: 654)
03016138
COMPARATIVE GENOMIC HYBRIDIZATION (CGH)
FULL TEXT: 3528 lines

9/6/12 (Item 4 from file: 654)
02990978
METHOD OF DIAGNOSING PREDISPOSITION FOR ULCERATIVE COLITIS IN JEWISH POPULATION BY DETECTION OF INTERLEUKIN-1 RECEPTOR ANTAGONIST **POLYMORPHISM**
FULL TEXT: 612 lines

9/6/13 (Item 5 from file: 654)
02983945
DETECTION OF HYPERMUTABLE NUCLEIC ACID SEQUENCE IN TISSUE
FULL TEXT: 1815 lines

9/6/14 (Item 6 from file: 654)
02934815
POLYMORPHIC LOCUS
FULL TEXT: 874 lines

9/6/15 (Item 7 from file: 654)
02922010
DIAGNOSIS OF DEPRESSION BY LINKAGE OF A POLYMORPHIC MARKER TO A SEGMENT OF CHROMOSOME 19P13 BORDERED BY D19S247 AND D19S394
FULL TEXT: 1466 lines

9/6/16 (Item 8 from file: 654)
02901617
TRABECULAR MESHWORK INDUCED GLUCOCORTICOID RESPONSE (TIGR) NUCLEIC ACID MOLECULES
[Accurate glaucoma diagnosis]
FULL TEXT: 1373 lines

9/6/17 (Item 9 from file: 654)
02895578
POLYMORPHISMS IN THE GLUCOSE-6 PHOSPHATE DEHYDROGENASE LOCUS
FULL TEXT: 1360 lines

9/6/18 (Item 10 from file: 654)
02895571
COMPARATIVE GENOMIC HYBRIDIZATION (CGH)
[Detection of amplification, reproduction, and, or deletion of genones]
FULL TEXT: 3541 lines

9/6/19 (Item 11 from file: 654)
02893542
METHODS FOR THE DIAGNOSIS OF GLAUCOMA
FULL TEXT: 1532 lines

9/6/20 (Item 12 from file: 654)
02893131
METHOD OF CHARACTERISATION OF GENOMIC DNA
FULL TEXT: 4623 lines

9/6/21 (Item 13 from file: 654)
02888348
METHODS FOR THE DIAGNOSIS OF GLAUCOMA
FULL TEXT: 1514 lines

9/6/22 (Item 14 from file: 654)
02846423
METHOD OF CHARACTERISATION
[Amplification of tandemly repeated region of genomic DNA, separation of set of amplification products to provide sample code]
FULL TEXT: 3543 lines

9/6/23 (Item 15 from file: 654)
02822670
METHODS FOR THE DIAGNOSIS OF GLAUCOMA
[Using a glucocorticoid induced protein]
FULL TEXT: 1949 lines

9/6/24 (Item 16 from file: 654)
02750443
COMPARATIVE GENOMIC HYBRIDIZATION
[Detecting abnormal nucleic acid sequence copy numbers in cell population]
FULL TEXT: 2854 lines

9/6/25 (Item 17 from file: 654)
02740190
METHOD OF SELECTING GENETICALLY SUPERIOR SHRIMP
[Screening shrimp and genetic marking, hybridization and isolation of DNA]
FULL TEXT: 791 lines

9/6/26 (Item 18 from file: 654)
02687789
COMPARATIVE GENOMIC HYBRIDIZATION (CGH)
[Labelling DNA sequences, hybridization; diagnosing genetic disorders]
FULL TEXT: 2975 lines

9/6/27 (Item 19 from file: 654)
02623272
METHODS FOR THE DIAGNOSIS OF GLAUCOMA
[Specific nucleic acid encoded human trabecular meshwork induced glucocorticoid response protein]
FULL TEXT: 1303 lines

9/6/28 (Item 20 from file: 654)
02409494
GENETIC IDENTIFICATION EMPLOYING DNA PROBES OF **VARIABLE NUMBER TANDEM REPEAT** LOCI
FULL TEXT: 2125 lines

9/6/29 (Item 21 from file: 654)
02404991

GENETIC DIAGNOSIS OF TORSION DYSTONIA
FULL TEXT: 2379 lines

9/6/30 (Item 22 from file: 654)
02357021
DNA TYPING WITH SHORT TANDEM REPEAT POLYMORPHISMS AND IDENTIFICATION OF POLYMORPHIC SHORT TANDEM REPEATS
FULL TEXT: 1738 lines

9/6/31 (Item 23 from file: 654)
01913496
GENETIC IDENTIFICATION EMPLOYING DNA PROBES OF **VARIABLE NUMBER TANDEM REPEAT** LOCI
[IDENTIFICATION OF CLONED DNA SEQUENCES]
FULL TEXT: 2145 lines
? t s9/7/1-7

9/7/1 (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

10019865 99303259
Characterization of a **variable number tandem repeat** region in the thiopurine S-methyltransferase gene promoter.
Spire-Vayron de la Moureyre C; Debuysere H; Fazio F; Sergent E; Bernard C ; Sabbagh N; Marez D; Lo Guidice JM; D'halluin JC; Broly F
Laboratoire de Biochimie et Biologie Moleculaire, Hopital Calmette, Centre Hospitalier Regional et Universitaire, Lille, France.
Pharmacogenetics (ENGLAND) Apr 1999, 9 (2) p189-98, ISSN 0960-314X Journal Code: BRT
Languages: ENGLISH
Document type: JOURNAL ARTICLE
Characterization of the genetic **polymorphism** of thiopurine S-methyltransferase enzyme (TPMT; EC 2.1.1.67) is required because of its clinical importance for patients exposed to thiopurine drugs. A number of point mutations have already been characterized in exons and introns of the TPMT gene. Here we report the identification of a polymorphic locus within the promoter region of the gene. This **polymorphism** was detected by polymerase chain reaction - single strand conformation **polymorphism** analysis of DNA samples from 54 unrelated European individuals. A total of five alleles with length variations were distinguished through the 5'-**flanking** region involved in the TPMT gene expression. Sequence analysis revealed that these variations were due to a variable number of tandem repeats (VNTR), ranging from four to eight repeats. Each repeat consists of 17 or 18 bp units and contains putative binding sites for transcription factors. The most frequent alleles harbour four or five tandem repeats, a heterozygosity rate of 0.44 was calculated, and a stable Mendelian inheritance of alleles was demonstrated. Analysis of the effect of each VNTR allele on promoter activity of a reporter gene was further performed in various cell lines by transient transfection assay. A modulatory effect of VNTR alleles was observed in vitro, but the repeat **polymorphism** did not display a significative role in TPMT gene regulation in vivo. Further studies need to be carried out to support the hypothesis that VNTR may contribute to the large interindividual variations of TPMT activity.

9/7/2 (Item 2 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09296867 97449816

Products of partial digestion with Hae III. Part ' Characterization, casework experience confirmation of the theory three-, four- and five-banded RFLP pattern origins using partial digestion.

Benzinger EA; Emerek EA; Grigsby NL; Duewer DL; Lovekamp ML; Deadman H; Thompson JL; Sallee PJ; Riech AK

Illinois State Police, Springfield, USA.

J Forensic Sci (UNITED STATES) Sep 1997, 42 (5) p850-63, ISSN 0022-1198 Journal Code: I5Z

Languages: ENGLISH

Document type: JOURNAL ARTICLE

The sizes of Hae III partial digestion products at D1S7, D2S44, D4S139, D5S110, D10S28, and D17S26 were evaluated in experimentally generated partial digestions of liquid blood DNA. The partial digestion products were highly predictable, suggesting a very high level of sequence conservation in regions **flanking variable number tandem repeat** (VNTR) blocks. Partial digestion bands associated with three-or-more-banded patterns were also characterized. Partial digestion of three-banded patterns can be used to determine whether the extra bands arise due to internal Hae III sites in the VNTR block and to identify hidden three-banded patterns. Partial digestion products from forensic casework also conformed to size expectations. Presumed partial digestion bands from 27 forensic samples were compared to the experimentally generated data. The causes of partial digestion are examined and recommendations for interpreting forensic DNA evidence exhibiting partial digestion products are given.

5, 7, 9, 14-20

9/7/3 (Item 3 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06500589 91033793

Rapid diagnosis of Miller-Dieker syndrome and isolated lissencephaly sequence by the polymerase chain reaction.

Batanian JR; Ledbetter SA; Wolff RK; Nakamura Y; White R; Dobyns WB; Ledbetter DH

Institute for Molecular Genetics, Baylor College of Medicine, Houston, TX 77030.

Hum Genet (GERMANY) Oct 1990, 85 (5) p555-9, ISSN 0340-6717 Journal Code: GED

Contract/Grant No.: HD20619, HD, NICHD

Languages: ENGLISH

Document type: JOURNAL ARTICLE

Probe YNZ22 (D17S5) is a highly polymorphic, **variable number tandem repeat** (VNTR) marker previously shown to be deleted in all patients with the Miller-Dieker syndrome (MDS) but not in patients with isolated lissencephaly sequence (ILS). Primers were constructed to the unique sequence **flanking** the polymorphic, repetitive region of YNZ22 for amplification by the polymerase chain reaction (PCR). Analysis of 118 normal individuals revealed 12 alleles (differing in copy number of a 70-bp repeat unit) ranging in size from 168 to 938 bp. A retrospective study of eight MDS and six ILS patients was consistent with Southern blot analysis in all cases except one. In the latter, a very large allele (12 copies of the repeat unit) in a patient and her mother failed to amplify on initial attempts, but was successfully amplified by reducing the concentration of genomic DNA used in the reaction. Prospective studies on two MDS and five ILS patients were successfully performed and confirmed in all cases by Southern blot analysis. From the total sample, restriction fragment length **polymorphism** (RFLP) analysis was fully informative in four of ten MDS patients and showed a deletion in all four cases. Nine of eleven ILS patients were heterozygous and therefore not deleted for YNZ22. Development of primers for additional polymorphic markers in the Miller-Dieker region will lead to a rapid PCR-based diagnostic approach for all MDS and ILS patients. PCR typing of YNZ22 will also facilitate use of this marker in other applications, including genetic linkage, paternity and forensic

studies, and analysis of loss of heterozygosity in tumo

9/7/4 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

12198641 BIOSIS NO.: 199900493490
Characterization of a **variable number tandem repeat** region in the thiopurine S-methyltransferase gene promoter.
AUTHOR: de la Moureyre Catherine Spire-Vayron; Debuysere Herve; Fazio Fanny ; Sergent Elodie; Bernard Claudine; Sabbagh Nada; Marez Delphine; Guidice Jean-Marc Lo; D'halluin Jean-Claude; Broly Franck(a)
AUTHOR ADDRESS: (a)Laboratoire de Biochimie et Biologie Moleculaire Hopital Calmette, CHRU de Lille, Boulevard Leclercq, F-59037, Lille Cedex**France
JOURNAL: Pharmacogenetics 9 (2):p189-198 April, 1999
ISSN: 0960-314X
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

ABSTRACT: Characterization of the genetic **polymorphism** of thiopurine S-methyltransferase enzyme (TPMT; EC 2.1.1.67) is required because of its clinical importance for patients exposed to thiopurine drugs. A number of point mutations have already been characterized in exons and introns of the TMPT gene. Here we report the identification of a polymorphic locus within the promoter region of the gene. This **polymorphism** was detected by polymerase chain reaction - single strand conformation **polymorphism** analysis of DNA samples from 54 unrelated European individuals. A total of five alleles with length variations were distinguished through the 5'-**flanking** region involved in the TPMT gene expression. Sequence analysis revealed that these variations were due to a variable number of tandem repeats (VNTR), ranging from four to eight repeats. Each repeat consists of 17 or 18 bp units and contains putative binding sites for transcription factors. The most frequent alleles harbour four or five tandem repeats, a heter ozygosity rate of 0.44 was calculated, and a stable Mendelian inheritance of alleles was demonstrated. Analysis of the effect of each VNTR allele on promoter activity of a reporter gene was further performed in various cell lines by transient transfection assay. A modulatory effect of VNTR alleles was observed in vitro, but the repeat **polymorphism** did not display a significative role in TPMT gene regulation in vivo. Further studies need to be carried out to support the hypothesis that VNTR may contribute to the large interindividual variations of TPMT activity.

9/7/5 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

08726704 BIOSIS NO.: 199395016055
Characterization of a porcine **variable number tandem repeat** sequence specific for the glucosephosphate isomerase locus.
AUTHOR: Davies W(a); Kran S; Kristensen T; Harbitz I
AUTHOR ADDRESS: (a)Dep. Biochem., Norw. Coll. Vet. Med., P.O. Box 8146 Dep, 0033 Oslo 1**Norway
JOURNAL: Animal Genetics 23 (5):p437-441 1992
ISSN: 0268-9146
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: A variable number of tandem repeat from a porcine glucosephosphate isomerase intron has been isolated and sequenced. The

repeat has a unit size of 39 bp, is highly conserved and is present in at least 14 copies. **Flanking** sequences show a sequence periodicity of 53-54 bp and some sequence homology to the 39 bp repeat. A considerable part of the genomic DNA has been lost during subcloning and is considered to be deletion prone or refractory to propagation in Escherichia coli. The tandem repeat is locus specific and detects at least six alleles in BamHI digested porcine DNA. No homology to other tandem repeat sequences has been found.

9/7/6 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

07331090 BIOSIS NO.: 000090110992
RAPID DETECTION OF HYPERVARIABLE REGIONS BY THE POLYMERASE CHAIN REACTION TECHNIQUE
AUTHOR: DECORTE R; CUPPENS H; MARYNEN P; CASSIMAN J-J
AUTHOR ADDRESS: CENTER HUMAN GENETICS, UNIV. LEUVEN, CAMPUS GASTHUISBERG O AND N6, HERESTRAAT, B-3000 LEUVEN, BELGIUM.
JOURNAL: DNA CELL BIOL 9 (6). 1990. 461-469.
CODEN: DCEBE
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The polymerase chain reaction (PCR) technique has provided a substantial improvement for the detection and analysis of known genetic polymorphisms. Here, we describe the application of this method for the detection of variable number of tandem repeat (VNTR) sequences. With the use of unique oligonucleotide primers, **flanking** the repeat sequence, and the thermostable Taq DNA polymerase, the hypervariable regions 3' of the Ha-ras gene, 3' of the apolipoprotein B gene, and 5' to the joining segments of the heavy-chain immunoglobulin gene could be amplified. Alleles up to 2,000 bp could be visualized directly on ethidium bromide-stained agarose gels. Larger alleles were seen only after traditional Southern blot analysis with an internal probe. The value of this new approach for the detection of VNTRs is illustrated in a case of paternity dispute.

9/7/7 (Item 1 from file: 399)
DIALOG(R)File 399:CA SEARCH(R)

116035667 CA: 116(5)35667p PATENT
DNA sequences from specific human genomic loci useful for identification of individuals
INVENTOR(AUTHOR): Keith, Tim P.; Mao, Jen I; Rose, Stanley D.
LOCATION: USA
ASSIGNEE: Collaborative Research, Inc.
PATENT: PCT International ; WO 9110748 A1 DATE: 910725
APPLICATION: WO 91US196 (910109) *US 464960 (900116)
PAGES: 49 pp. CODEN: PIXXD2 LANGUAGE: English CLASS: C12Q-001/70A; C07H-021/04B; G01N-033/53B DESIGNATED COUNTRIES: AU; CA; JP
DESIGNATED REGIONAL: AT; BE; CH; DE; DK; ES; FR; GB; GR; IT; LU; NL; SE
SECTION:
CA203005 Biochemical Genetics
IDENTIFIERS: oligonucleotide primer DNA VNTR region, hybridization probe DNA VNTR region, human chromosome VNTR primer probe, variable number tandem repeat chromosome primer
DESCRIPTORS:
Nucleotides,oligo-,polymers...
as primers and probes for human chromosome variable no. of tandem repeat regions in DNA identity detn.
Genetic polymorphism...

at variable no. tandem repeat loci, in detn. of DNA sample identities
Gene,animal...
D1S47, variable no. tandem repeats in, polymorphism of, detn. of, in DNA sample identity detn.
Gene,animal...
D11S129, variable no. tandem repeats in, polymorphism of, detn. of, in DNA sample identity detn.
Gene,animal...
D18S17, variable no. tandem repeats in, polymorphism of, detn. of, in DNA sample identity detn.
Gene,animal...
D20S112, variable no. tandem repeats in, polymorphism of, detn. of, in DNA sample identity detn.
Gene,animal...
D20S15, variable no. tandem repeats in, polymorphism of, detn. of, in DNA sample identity detn.
Gene,animal...
D6S22, variable no. tandem repeats in, polymorphism of, detn. of, in DNA sample identity detn.
Deoxyribonucleic acid sequences...
of human chromosome 11 variable no. of tandem repeat locus D11S129, oligonucleotide primers and probes for DNA identity detn. in relation to
Deoxyribonucleic acid sequences...
of human chromosome 6 variable no. of tandem repeat locus D6S22, oligonucleotide primers and probes for DNA identity detn. in relation to
Nucleic acid hybridization...
oligonucleotide probes for, for human chromosome variable no. of tandem repeat regions in DNA identity detn.
Deoxyribonucleic acids...
polymerase chain reaction amplification of, oligonucleotide primers for, for human chromosome variable no. of tandem repeat regions in DNA identity detn.
Gene,animal...
variable no. of tandem repeat (VNTR), of human chromosomes, oligonucleotide primer and probes for, for DNA identity detn.
Chromosome,human 1... Chromosome,human 11... Chromosome,human 18...
Chromosome,human 20... Chromosome,human 21... Chromosome,human 6...
variable no. of tandem repeat region and flanking sequences of, oligonucleotide primers and probes for, DNA identity detn. in relation to
CAS REGISTRY NUMBERS:
138363-06-1 138363-07-2 as oligonucleotide primer for sizing of variable amt. of tandem repeat alleles at human chromosome 20 locus D20S15
138363-08-3 138363-09-4 nucleotide sequence of, oligonucleotide primers and probes for DNA identity detn. in relation to
? t s9/3,ab/22, 28, 30, 31

9/3,AB/22 (Item 14 from file: 654)
DIALOG(R)File 654:US Pat.Full.

02846423
Utility
METHOD OF CHARACTERISATION
[Amplification of tandemly repeated region of genomic DNA, separation of set of amplification products to provide sample code]

PATENT NO.: 5,811,235
ISSUED: September 22, 1998 (19980922)
INVENTOR(s): Jeffreys, Alec John, Leicester, GB (United Kingdom).England
ASSIGNEE(s): Zeneca Limited, (A Non-U.S. Company or Corporation), London, GB (United Kingdom) England

[Assignee Code(s): 32757]
APPL. NO.: 8-418,859
FILED: April 05, 1995 (19950405)
PRIORITY: 9118371, GB (United Kingdom), August 27, 1991 (19910827)
9119089, GB (United Kingdom), September 6, 1991 (19910906)
9124636, GB (United Kingdom), November 20, 1991 (19911120)
9207379, GB (United Kingdom), April 3, 1992 (19920403)
9212627, GB (United Kingdom), June 15, 1992 (19920615)
9212881, GB (United Kingdom), June 17, 1992 (19920617)

This is a continuation of application Ser. No. 07-935,107, filed Aug. 26, 1992, now abandoned.

FULL TEXT: 3543 lines

ABSTRACT

A method of characterizing a test sample of genomic DNA which method comprises amplifying a tandemly repeated region, comprising more than one type of repeat unit, as far as internal repeat units of a specific type so as to generate a set of amplification products which identify the relative positions of the internal repeat units within the tandemly repeated region, and separating the set of amplification products to provide a sample code. The sample codes are suitable for computerized storage on, and retrieval from, a database. The invention also provides a novel method for the detection of diagnostic base sequences in one or more nucleic acids contained in a sample.

9/3,AB/28 (Item 20 from file: 654)
DIALOG(R)File 654:US Pat.Full.

02409494

Utility
GENETIC IDENTIFICATION EMPLOYING DNA PROBES OF **VARIABLE NUMBER TANDEM REPEAT** LOCI

PATENT NO.: 5,411,859
ISSUED: May 02, 1995 (19950502)
INVENTOR(s): White, Raymond L., Salt Lake City, UT (Utah), US (United States of America)
Nakamura, Yusuke, Salt Lake City, UT (Utah), US (United States of America)
O'Connell, Peter, Salt Lake City, UT (Utah), US (United States of America)
Midvale, Salt Lake City, UT (Utah), US (United States of America)
Leppert, Mark F., Salt Lake City, UT (Utah), US (United States of America)
ASSIGNEE(s): University of Utah Research Foundation, (A U.S. Company or Corporation), Salt Lake City, UT (Utah), US (United States of America)
[Assignee Code(s): 88042]
EXTRA INFO: Assignment transaction [Reassigned], recorded April 29, 1998 (19980429)
Assignment transaction [Reassigned], recorded February 26, 1999 (19990226)
APPL. NO.: 7-728,751
FILED: June 10, 1991 (19910610)

CROSS REFERENCE TO RELATED APPLICATION

This application is a continuation of application Ser. No. 07-597,039,

filed Oct. 15, 1990, now abandoned, which is divisional of application Ser. No. 07-307,820, filed Feb. 8, 1989, now U.S. Pat. No. 4,963,663, which is a continuation-in-part of application Ser. No. 07-288,835, filed Dec. 23, 1988, now abandoned, which is a continuation-in-part of application Ser. No. 07-282,141, filed Dec. 9, 1988, now abandoned, which is a continuation-in-part of application Ser. No. 07-157,962, filed Feb. 18, 1988, now abandoned.

FULL TEXT: 2125 lines

ABSTRACT

The present invention is related to the identification of cloned DNA sequences that reveal individual multiallele loci. The loci are used in the process of the present invention to provide convenient and accurate genetic identification. A large number of clones that recognize VNTR loci have been isolated from a cosmid library and characterized.

9/3,AB/30 (Item 22 from file: 654)
DIALOG(R)File 654:US Pat.Full.

02357021

Utility

DNA TYPING WITH SHORT TANDEM REPEAT POLYMORPHISMS AND IDENTIFICATION OF POLYMORPHIC SHORT TANDEM REPEATS

PATENT NO.: 5,364,759
ISSUED: November 15, 1994 (19941115)
INVENTOR(s): Caskey, Charles T., Houston, TX (Texas), US (United States of America)
Edwards, Albert O., Houston, TX (Texas), US (United States of America)
ASSIGNEE(s): Baylor College of Medicine, (A U.S. Company or Corporation), Houston, TX (Texas), US (United States of America)
[Assignee Code(s): 6345]
EXTRA INFO: Reexamined, certified November 18, 1997 (19971118)
Reexamined, certified July 20, 1999 (19990720)
APPL. NO.: 7-647,655
FILED: January 31, 1991 (19910131)

FULL TEXT: 1738 lines

ABSTRACT

The present invention relates to a DNA profiling assay for detecting polymorphisms in a short tandem repeat. The method includes the steps of extracting DNA from a sample to be tested, amplifying the extracted DNA and identifying the amplified extension products for each different sequence. Each different sequence is differentially labeled. In the method, internal and external standards can also be used. The method is applicable to a wide variety of forensic and medical samples, including blood, semen, vaginal swaps, tissue, hair, saliva, urine and mixtures of body fluids. A short tandem repeat sequence which can be characterized by the formula (A sub w G sub x T sub y C sub z) sub n, wherein A, G, T and C represent the nucleotides, w, x, y and z represent the number of nucleotide and range from 0 to 7 and the sum of w+x+y+z ranges from 3 to 7 and n represents the repeat number and ranges from 5 to 50. The labels can be from a variety of groups, including fluorescers, radioisotopes, chemiluminescers, stains, enzymes and antibodies. Also described is a kit. Further, a method of detecting the polymorphic short tandem repeats comprising the steps of either searching for the repeats in a data base or comparing

oligonucleotides and searching for the repeats in a genomic library.

9/3,AB/31 (Item 23 from file: 654)
DIALOG(R)File 654:US Pat.Full.

01913496

Utility
GENETIC IDENTIFICATION EMPLOYING DNA PROBES OF **VARIABLE NUMBER TANDEM REPEAT** LOCI
[IDENTIFICATION OF CLONED DNA SEQUENCES]

PATENT NO.: 4,963,663
ISSUED: October 16, 1990 (19901016)
INVENTOR(s): White, Raymond L., Salt Lake City, UT (Utah), US (United States of America)
Nakamura, Yusuke, Salt Lake City, UT (Utah), US (United States of America)
O'Connell, Peter, Midvale, UT (Utah), US (United States of America)
Leppert, Mark F., Salt Lake City, UT (Utah), US (United States of America)
ASSIGNEE(s): University of Utah, (A U.S. Company or Corporation), Salt Lake City, UT (Utah), US (United States of America)
[Assignee Code(s): 88042]
EXTRA INFO: Assignment transaction [Reassigned], recorded March 3, 1992 (19920303)
Assignment transaction [Reassigned], recorded April 29, 1998 (19980429)
Assignment transaction [Reassigned], recorded February 26, 1999 (19990226)
APPL. NO.: 7-307,820
FILED: February 08, 1989 (19890208)

CROSS REFERENCE TO RELATED APPLICATION

This application is a continuation-in-part of application Ser. No. 288,835, filed Dec. 23, 1988 which is a continuation-in-part of application Ser. No. 282,141, filed Dec. 9, 1988 which is a continuation-in-part of application Ser. No. 157,962 filed Feb. 18, 1988.

FULL TEXT: 2145 lines

ABSTRACT

The present invention is related to the identification of cloned DNA sequences that reveal individual multiallele loci. The loci are used in the process of the present invention to provide convenient and accurate genetic identification. A large number of clones that recognize VNTR loci have been isolated from a cosmid library and characterized.
? ds

Set	Items	Description
S1	1	AU="FIRTH, GREG"
S2	5	AU="FIRTH, G."
S3	461	VARIABLE(W)NUMBER(W)TANDEM(W)REPEAT
S4	2	VARIABLE(W)NUMBER(W)TANDEM(W)REPEAT(W)ALLELE
S5	2	RD (unique items)
S6	1	S1 AND POLYMORPHISM
S7	252	S3 AND POLYMORPHISM
S8	34	S7 AND FLANKING

S9 31 RD (unique items)
? s amplimer

S10 438 AMPLIMER
? s s10 and s3

438 S10
461 S3
S11 2 S10 AND S3
? t s11/6/1-2

11/6/1 (Item 1 from file: 654)
02893131
METHOD OF CHARACTERISATION OF GENOMIC DNA
FULL TEXT: 4623 lines

11/6/2 (Item 2 from file: 654)
02846423
METHOD OF CHARACTERISATION
[Amplification of tandemly repeated region of genomic DNA, separation of set of amplification products to provide sample code]
FULL TEXT: 3543 lines
?

? t s11/3,ab/1-2

11/3,AB/1 (Item 1 from file: 654)
DIALOG(R)File 654:US Pat.Full.

02893131
Utility
METHOD OF CHARACTERISATION OF GENOMIC DNA

PATENT NO.: 5,853,989
ISSUED: December 29, 1998 (19981229)
INVENTOR(s): Jeffreys, Alec John, Leicester, GB (United Kingdom).Great Britian
Little, Stephen, Chester, GB (United Kingdom).Great Britian
Ferrie, Richard Mark, Cheshire, GB (United Kingdom).Great Britian
Brownie, Jannine, Cheshire, GB (United Kingdom).Great Britian
ASSIGNEE(s): Zeneca Limited, (A Non-U.S. Company or Corporation), London, GB (United Kingdom)
[Assignee Code(s): 32757]
APPL. NO.: 8-643,181
FILED: May 06, 1996 (19960506)
PRIORITY: 9118371, GB (United Kingdom), August 27, 1991 (19910827)
9119089, GB (United Kingdom), September 6, 1991 (19910906)
9124636, GB (United Kingdom), November 20, 1991 (19911120)
9207379, GB (United Kingdom), April 3, 1992 (19920403)
9212627, GB (United Kingdom), June 15, 1992 (19920615)
9212881, GB (United Kingdom), June 17, 1992 (19920617)

This application is a continuation-in-part of application of Ser. No. 08-418,859 filed Apr. 5, 1995 which is a continuation of 07-935,107, filed Aug. 26, 1992 now abandoned.

FULL TEXT: 4623 lines

ABSTRACT

The present invention relates generally to a method of characterizing a sample of genomic DNA and to nucleotide sequences employed in the method as well as kits comprising these. In particular the invention involves the use of primers which selectively prime specific type(s) of internal repeat unit in a tandemly repeated region. The method of the invention is particularly useful in forensic or paternity studies and provides individual sample codes suitable for computerized storage on, and retrieval from, a database.

11/3,AB/2 (Item 2 from file: 654)
DIALOG(R)File 654:US Pat.Full.

02846423

Utility
METHOD OF CHARACTERISATION
[Amplification of tandemly repeated region of genomic DNA, separation of set of amplification products to provide sample code]

PATENT NO.: 5,811,235
ISSUED: September 22, 1998 (19980922)
INVENTOR(s): Jeffreys, Alec John, Leicester, GB (United Kingdom).England
ASSIGNEE(s): Zeneca Limited, (A Non-U.S. Company or Corporation), London, GB (United Kingdom) England
[Assignee Code(s): 32757]
APPL. NO.: 8-418,859
FILED: April 05, 1995 (19950405)
PRIORITY: 9118371, GB (United Kingdom), August 27, 1991 (19910827)
9119089, GB (United Kingdom), September 6, 1991 (19910906)
9124636, GB (United Kingdom), November 20, 1991 (19911120)
9207379, GB (United Kingdom), April 3, 1992 (19920403)
9212627, GB (United Kingdom), June 15, 1992 (19920615)
9212881, GB (United Kingdom), June 17, 1992 (19920617)
This is a continuation of application Ser. No. 07-935,107, filed Aug. 26, 1992, now abandoned.

FULL TEXT: 3543 lines

ABSTRACT

A method of characterizing a test sample of genomic DNA which method comprises amplifying a tandemly repeated region, comprising more than one type of repeat unit, as far as internal repeat units of a specific type so as to generate a set of amplification products which identify the relative positions of the internal repeat units within the tandemly repeated region, and separating the set of amplification products to provide a sample code. The sample codes are suitable for computerized storage on, and retrieval from, a database. The invention also provides a novel method for the detection of diagnostic base sequences in one or more nucleic acids contained in a sample.
? ds

Set	Items	Description
S1	1	AU="FIRTH, GREG"
S2	5	AU="FIRTH, G."
S3	461	VARIABLE(W)NUMBER(W)TANDEM(W)REPEAT
S4	2	VARIABLE(W)NUMBER(W)TANDEM(W)REPEAT(W)ALLELE
S5	2	RD (unique items)
S6	1	S1 AND POLYMORPHISM
S7	252	S3 AND POLYMORPHISM

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S8          34   S7 AND FLANKING
S9          31   RD (unique items)
S10        438   AMPLIMER
S11          2   S10 AND S3
? s s3 and genomic

             461  S3
          130463  GENOMIC
     S12      75  S3 AND GENOMIC
? rd

>>>Duplicate detection is not supported for File 654.

>>>Records from unsupported files will be retained in the RD set.
...examined 50 records  (50)
...completed examining records
     S13      61  RD (unique items)
? s s13 not s8

              61  S13
              34  S8
     S14      35  S13 NOT S8
? t s11/6/1-35


 11/6/1     (Item 1 from file: 654)
02893131
METHOD OF CHARACTERISATION OF GENOMIC DNA
FULL TEXT:         4623 lines


 11/6/2     (Item 2 from file: 654)
02846423
METHOD OF CHARACTERISATION
[ Amplification  of  tandemly repeated region of genomic DNA, separation of
set of amplification products to provide sample code]
FULL TEXT:         3543 lines
? t s14/6/1-35


 14/6/1     (Item 1 from file: 155)
10241122   20081706
  Analysis  of  parent-offspring  trios  provides  evidence for linkage and
association  between  the  insulin  gene  and  type  2  diabetes  mediated
exclusively  through  paternally  transmitted  class  III  variable
number tandem repeat alleles.
Jan 2000


 14/6/2     (Item 2 from file: 155)
09709628   98424414
   Duplication  of  a  genomic  region  containing  the  Cdc2L1-2 and
MMP21-22 genes on human chromosome 1p36.3 and their linkage to D1Z2.
Sep 1998


 14/6/3     (Item 3 from file: 155)
09081095   97311416
  Gene  organization  of human NOTCH4 and (CTG)n polymorphism in this human
counterpart gene of mouse proto-oncogene Int3.
Apr 21 1997


 14/6/4     (Item 4 from file: 155)
08927469   97147788
```

Genomic differentiation among natural populations of orang-utan (Pongo pygmaeus).
Oct 1 1996

14/6/5 (Item 5 from file: 155)
08820287 96432029
Two additional polymorphisms within the hypervariable MUC1 gene: association of alleles either side of the VNTR region.
Jan 1996

14/6/6 (Item 6 from file: 155)
08788942 96296999
Thyroid peroxidase: evidence for disease gene exclusion in Pendred's syndrome.
Apr 1996

14/6/7 (Item 7 from file: 155)
08195213 95078843
Early embryonic failure associated with uniparental disomy for human chromosome 21.
Aug 1994

14/6/8 (Item 8 from file: 155)
08090783 95113701
DNA fingerprinting used to test for family effects on precocious sexual maturation in two populations of Oncorhynchus tshawytscha (Chinook salmon).
Dec 1994

14/6/9 (Item 9 from file: 155)
08051141 95057304
No evidence for microsatellite instability or consistent loss of heterozygosity at selected loci in chronic myeloid leukaemia blast crisis.
Nov 1994

14/6/10 (Item 10 from file: 155)
07445472 93036587
Characterization of a porcine **variable number tandem repeat** sequence specific for the glucosephosphate isomerase locus.
1992

14/6/11 (Item 11 from file: 155)
07354599 91332029
Molecular cloning and analysis of the mouse homologue of the tumor-associated mucin, MUC1, reveals conservation of potential O-glycosylation sites, transmembrane, and cytoplasmic domains and a loss of minisatellite-like polymorphism.
Aug 15 1991

14/6/12 (Item 12 from file: 155)
07344347 90368715
Molecular cloning and expression of human tumor-associated polymorphic epithelial mucin.
Sep 5 1990

14/6/13 (Item 13 from file: 155)
07245699 93145050

Automated DNA profiling by fluorescent labeling of PCR products.
Aug 1992

14/6/14 (Item 14 from file: 155)
06824327 92043591
Analytical DNA fingerprinting in lions: parentage, genetic diversity, and kinship.
Sep-Oct 1991

14/6/15 (Item 15 from file: 155)
06374849 90196701
Use of multiallelic human DNA probes to detect polymorphisms in the porcine genome.
Mar 1990

14/6/16 (Item 16 from file: 155)
05811008 89372155
Enzymatic synthesis of DNA probes complementary to a human **variable number tandem repeat** locus.
Jun 1989

14/6/17 (Item 1 from file: 5)
11666796 BIOSIS NO.: 199800448527
VNTR (variable number of tandem repeat) sequences as transcriptional, translational, or functional regulators.
1998

14/6/18 (Item 2 from file: 5)
11521469 BIOSIS NO.: 199800302801
Genetic relationships among Japanese, Northern Han, Hui, Uygur, Kazakh, Greek, Saudi Arabian, and Italian populations based on allelic frequencies at four VNTR (D1S80, D4S43, COL2A1, D17S5) and one STR (ACTBP2) loci.
1998

14/6/19 (Item 3 from file: 5)
11006345 BIOSIS NO.: 199799627490
Usefulness of intron 40 variable number tandem repeats (VNTR) in gene tracking 14 families with type 1 and 3 von Willebrand disease.
1997

14/6/20 (Item 4 from file: 5)
10753435 BIOSIS NO.: 199799374580
DNA allelic alterations within VNTR loci of scleroderma families.
1996

14/6/21 (Item 5 from file: 5)
09036704 BIOSIS NO.: 199497045074
Hypervariable single and multi-locus DNA polymorphisms for genetic typing of non-human primates.
1993

14/6/22 (Item 6 from file: 5)
08947711 BIOSIS NO.: 199396099212
Parentage determination on placental tissues through deoxyribonucleic acid fingerprints.

1993

14/6/23 (Item 7 from file: 5)
07498879 BIOSIS NO.: 000091072748
STRUCTURE AND EXPRESSION OF THE HUMAN POLYMORPHIC EPITHELIAL MUCIN GENE AN EXPRESSED VNTR UNIT
1990

14/6/24 (Item 8 from file: 5)
06605822 BIOSIS NO.: 000087047984
A MAPPED SET OF GENETIC MARKERS FOR HUMAN CHROMOSOME 9
1988

14/6/25 (Item 1 from file: 357)
0201896 DBA Accession No.: 96-12667
Genetic typing by capillary electrophoresis with the allelic ladder as an absolute standard - **variable number tandem repeat** polymorphism detection 1996

14/6/26 (Item 2 from file: 357)
0148651 DBA Accession No.: 93-06703
A low profile - examination of the use of molecular biology in DNA fingerprinting forensics 1993

14/6/27 (Item 3 from file: 357)
0102806 DBA Accession No.: 90-05497
Alkaline transfer of small restriction fragments from polyacrylamide gels - Southern blot hybridization of DNA after polyacrylamide gel electrophoresis; application in **variable number tandem repeat** detection 1990

14/6/28 (Item 1 from file: 654)
02987652
METHOD FOR CAPTURING A NUCLEIC ACID
FULL TEXT: 826 lines

14/6/29 (Item 2 from file: 654)
02788987
COMPOSITIONS FOR CHROMOSOME-SPECIFIC STAINING
[Nucleic acid probes for in situ hybridization with labels]
FULL TEXT: 3373 lines

14/6/30 (Item 3 from file: 654)
02788602
SEQUENCE OF HUMAN DOPAMINE TRANSPORTER CDNA
FULL TEXT: 1776 lines

14/6/31 (Item 4 from file: 654)
02745507
VNTR PROBES AND METHODS OF USING THEREOF
[Genetic identification]
FULL TEXT: 679 lines

14/6/32 (Item 5 from file: 654)
02724581

DETECTING GENETIC PREDISPOSITION FOR OSTEOPOROSIS
[Isolation **genomic** Dn[redacted]determination allelic pattern]
FULL TEXT: 632 lines

14/6/33 (Item 6 from file: 654)
02588755
PROCESS OF SELECTING AND/OR OBTAINING PROBES CAPABLE OF DETECTING NEW **VARIABLE NUMBER TANDEM REPEAT** REGIONS
FULL TEXT: 727 lines

14/6/34 (Item 7 from file: 654)
02468366
PROCESS FOR TESTING GENE-DISEASE ASSOCIATIONS
FULL TEXT: 1131 lines

14/6/35 (Item 8 from file: 654)
02427349
REPEAT SEQUENCE CHROMOSOME SPECIFIC NUCLEIC ACID PROBES AND METHODS OF PREPARING AND USING
[Primer directed DNA amplification using degenerate primers to isolate efficiently chromosome-specific repeated DNA]
FULL TEXT: 2094 lines
? t s14/7/1-27

14/7/1 (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

10241122 20081706
Analysis of parent-offspring trios provides evidence for linkage and association between the insulin gene and type 2 diabetes mediated exclusively through paternally transmitted class III **variable number tandem repeat** alleles.
Huxtable SJ; Saker PJ; Haddad L; Walker M; Frayling TM; Levy JC; Hitman GA; O'Rahilly S; Hattersley AT; McCarthy MI
Division of Medicine, Imperial College School of Medicine, St. Mary's Hospital, London, UK.
Diabetes (UNITED STATES) Jan 2000, 49 (1) p126-30, ISSN 0012-1797 Journal Code: E8X
Languages: ENGLISH
Document type: JOURNAL ARTICLE
Variation at the **variable number tandem repeat** (VNTR) minisatellite 5' of the insulin gene (INS) is associated with several phenotypes, including type 1 diabetes, polycystic ovary syndrome, and birth weight. Case-control studies have suggested that class III VNTR alleles are also associated with type 2 diabetes, but results have been inconsistent and may reflect population stratification. To explore further the role of the INS-VNTR in type 2 diabetes susceptibility, we used family-based association methods in 155 parent-offspring trios from the British Diabetic Association-Warren Trios repository, each ascertained via a Europid proband with type 2 diabetes. Overall, there was no significant association between diabetes and the INS-VNTR genotype, with 65 of 119 heterozygous parents (55%) transmitting class III and 54 class I (P = 0.16, one-sided). However, whereas maternal transmissions followed Mendelian expectation, there was a marked excess of class III transmission from the 49 heterozygous fathers (34 [69%] vs. 15, P = 0.003 vs. 50% expectation, P = 0.003 vs. maternal transmission). These results confirm that variation within the TH-INS-IGF2 locus, most plausibly at the VNTR itself, influences type 2 diabetes susceptibility. By demonstrating that this effect is mediated exclusively by the paternally derived allele, these findings implicate imprinted genes in the pathogenesis of type 2 diabetes.

14/7/2 (Item 2 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09709628 98424414
Duplication of a **genomic** region containing the Cdc2L1-2 and MMP21-22 genes on human chromosome 1p36.3 and their linkage to D1Z2.
Gururajan R; Lahti JM; Grenet J; Easton J; Gruber I; Ambros PF; Kidd VJ
Department of Tumor Cell Biology, St. Jude Children's Research Hospital, Memphis, Tennessee 38101 USA.
Genome Res (UNITED STATES) Sep 1998, 8 (9) p929-39, ISSN 1088-9051 Journal Code: CES
Contract/Grant No.: GM44088, GM, NIGMS; CA67938, CA, NCI; CA21765, CA, NCI
Languages: ENGLISH
Document type: JOURNAL ARTICLE
Cdc2L1 and Cdc2L2 span approximately 140 kb on human chromosome 1p36.3. The products of the Cdc2L genes encode almost identical protein kinases, the PITSLRE kinases, which have functions that may be relevant to the regulation of transcription/splicing and apoptotic signaling. These genes are deleted/translocated in neuroblastomas with MYCN gene amplification, a subset of malignant melanomas, and in a newly delineated deletion syndrome. Here we report that the p36.3 region of human chromosome 1 consists of two identical **genomic** regions, each of which contain a Cdc2L gene linked to a metalloprotease (MMP) gene in a tail-to-tail configuration. This duplicated **genomic** region is also linked tightly to D1Z2, a genetic marker containing a highly polymorphic VNTR (**variable number tandem repeat**) consisting of an unusual 40-bp reiterated sequence. Thus, these genes and the polymorphic marker D1Z2 are organized as follows: telomere-D1Z2-5'-MMP22-3'-3'-Cdc2L2-5'-5'-Cdc2L1 -3'-3'-MMP21-5'-centromere. Remarkably, the introns and exons of Cdc2L1 and Cdc2L2, as well as their flanking regions, are essentially identical. A total of 15 amino acid differences, 12 nonconservative and 3 conservative, can be found in the 773-786 amino acids specified by the various products of the Cdc2L genes. Two separate promoter/5' untranslated (UT) regions, CpG1 and CpG2, are identical to a reported previously methylated **genomic** CpG sequence and are used to express >20 different Cdc2L transcripts from the two genes. The expression of CpG2 transcripts from Cdc2L1 and Cdc2L2 is tissue/cell-line specific. CpG1 transcripts are expressed ubiquitously from both genes, with perhaps some bias towards the expression of CpG1 Cdc2L1 mRNAs in certain hematopoietic cells.

14/7/3 (Item 3 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09081095 97311416
Gene organization of human NOTCH4 and (CTG)n polymorphism in this human counterpart gene of mouse proto-oncogene Int3.
Sugaya K; Sasanuma S; Nohata J; Kimura T; Fukagawa T; Nakamura Y; Ando A; Inoko H; Ikemura T; Mita K
Genome Research Group, National Institute of Radiological Sciences, Anagawa, Chiba-ken, Japan. k sugaya@uexs72.nirs.go.jp
Gene (NETHERLANDS) Apr 21 1997, 189 (2) p235-44, ISSN 0378-1119 Journal Code: FOP
Languages: ENGLISH
Document type: JOURNAL ARTICLE
The cDNA and **genomic** clones for the human counterpart of the mouse mammary tumor gene Int3 were isolated and sequenced. We designated this human major histocompatibility complex (MHC) class III gene as NOTCH4, since very recently, by sequencing cDNA clones, the complete form of the mouse proto-oncogene Int3 has been clarified and named Notch4. The present

human NOTCH4 sequence is the first example of the **genomic** sequence for the extracellular portion of the mammalian Notch4 gene and by comparing it with the mouse Notch4 cDNA sequence, the exon/intron organization was clarified. The comparison of the predicted amino acid sequence of human NOTCH4 with those of other Notch homologues of a wide range of species revealed four subfamilies for mammalian Notch. In the protein coding region of human NOTCH4, we found (CTG)n repeats showing a **variable number tandem repeat** (VNTR) polymorphism for different human leukocyte antigen (HLA) haplotypes. Ten genes mapped on 6p21.3, including NOTCH4, were found to have counterparts structurally and functionally similar to those mostly mapped on 9q33-q34, indicating segmental chromosome duplication during the course of evolution. Similarity of genes on chromosomes 1, 6, 9 and 19 was also discussed.

14/7/4 (Item 4 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08927469 97147788

Genomic differentiation among natural populations of orang-utan (Pongo pygmaeus).

Zhi L; Karesh WB; Janczewski DN; Frazier-Taylor H; Sajuthi D; Gombek F; Andau M; Martenson JS; O'Brien SJ

Laboratory of Genomic Diversity, National Cancer Institute, Frederick, Maryland 21702-1201, USA.

Curr Biol (ENGLAND) Oct 1 1996, 6 (10) p1326-36, ISSN 0960-9822 Journal Code: B44

Languages: ENGLISH

Document type: JOURNAL ARTICLE

BACKGROUND: Orang-utans exist today in small isolated populations on the islands of Borneo (subspecies Pongo pygmaeus pygmaeus) and Sumatra (subspecies P. p. abelii). Although, on the basis of their morphological, behavioral and cytogenetical characteristics, the Bornean and Sumatran orang-utan populations are generally considered as two separate subspecies, there is no universal agreement as to whether their genetic differentiation is sufficient to consider and manage them as species, subspecies or population level taxonomic units. A more precise phylogenetic description would affect many conservation management decisions about captive and free-ranging orang-utans. RESULTS: We analyzed the amount and patterns of molecular genetic variation in orang-utan populations using cellular DNA from orang-utans from two locations in Sumatra and nine locations-representing four isolated populations-in Borneo. Genetic and phylogenetic analyses of mitochondrial DNA restriction fragment length polymorphisms, nuclear minisatellite (or **variable number tandem repeat**) loci and mitochondrial 16S ribosomal RNA sequences led to three major findings. First, the genetic distance and phylogenetic differentiation between Sumatran and Bornean orang-utans is large, greater than that between the common chimpanzee, Pan troglodytes, and the pygmy chimpanzee or bonobo, Pan paniscus. The genetic distance suggests that the two island subspecies diverged approximately 1.5-1.7 million years ago, well before the two islands separated and long enough for species-level differentiation. Second, there is considerable endemic genetic diversity within the Bornean and Sumatran orang-utan populations, suggesting that they have not experienced recent bottlenecks or founder effects. And third, there is little genetic differentiation among four geographically isolated populations of Bornean orang-utans, consistent with gene flow having occurred between them until recently. CONCLUSIONS: Our results are consistent with the view that the genetic differentiation between Sumatran and Bornean orang-utans has reached the level of distinct species. Furthermore, our findings indicate that there is not a genetic imperative for the separate management of geographically isolated Bornean populations.

14/7/5 (Item 5 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2000 Dialog Corporation. All rts. reserv.

08820287 96432029
Two additional polymorphisms within the hypervariable MUC1 gene: association of alleles either side of the VNTR region.
Pratt WS; Islam I; Swallow DM
MRC Human Biochemical Genetics Unit, Galton Laboratory (UCL), London, U.K.
Ann Hum Genet (ENGLAND) Jan 1996, 60 (Pt 1) p21-28, ISSN 0003-4800 Journal Code: 58C
Languages: ENGLISH
Document type: JOURNAL ARTICLE
The gene MUC1 codes for a mucin-type glycoprotein and like most of the other mucin genes shows **variable number tandem repeat** (VNTR) polymorphism within the coding region. A polymorphism due to a G/A substitution in exon 2, responsible for a genetically determined variation in splicing of the MUC1 transcript, has also been reported (Ligtenberg et al. 1990, 1991). Here we describe the detection of this nucleotide substitution polymorphism by single stranded conformational analysis of **genomic** DNA and we also report a CA repeat polymorphism within intron 6 of the gene. Haplotypes were determined in a series of families and the common alleles of these two polymorphisms were found to be associated. These results support the notion that the VNTR polymorphism in the coding sequence of MUC1 is not caused by unequal reciprocal recombination at meiosis.

14/7/6 (Item 6 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2000 Dialog Corporation. All rts. reserv.

08788942 96296999
Thyroid peroxidase: evidence for disease gene exclusion in Pendred's syndrome.
Gausden E; Armour JA; Coyle B; Coffey R; Hochberg Z; Pembrey M; Britton KE; Grossman A; Reardon W; Trembath R
Department of Genetics, University of Leicester, UK.
Clin Endocrinol (Oxf) (ENGLAND) Apr 1996, 44 (4) p441-6, ISSN 0300-0664 Journal Code: DCI
Languages: ENGLISH
Document type: JOURNAL ARTICLE
OBJECTIVE: Pendred's syndrome is an association between congenital neurosensory deafness and goitre with abnormal discharge of iodide following perchlorate challenge, indicating a defect of iodide organification. Although Pendred's syndrome may cause up to 7.5% of all cases of congenital deafness, the molecular basis of the association between the hearing loss and the thyroid organification defect remains unknown. We chose to investigate the role of the thyroid peroxidase (TPO) gene as the genetic defect in Pendred's syndrome. DESIGN: A highly informative **variable number tandem repeat** (VNTR), located 1.5 kb downstream of exon 10 of the TPO gene, was used to search for genetic linkage in multiple sibships affected by Pendred's syndrome. PATIENTS: Seven kindreds were recruited from the UK, each with at least two affected members. We have also examined a large inbred Israeli family with two affected offspring and five unaffected children. MEASUREMENTS: Individuals were assigned affected status based on the characteristic clinical features of Pendred's syndrome, namely the presence of congenital sensorineural hearing loss and the appearance in early life of a goitre. Additionally, at least one affected member from each sibship had a characteristic positive perchlorate discharge test (Morgans & Trotter, 1958). PCR amplification of **genomic** DNA at the TPO VNTR allowed assignment of genotypes to each individual and the calculation of a two-point LOD score. RESULTS: In six of the nine sibships analysed we found

obligatory recombination between TPO and Pendred's syndrome. Non-complementation observed in affected parents with affected offspring excluded TPO in an affected sibship with genotype sharing and supports a hypothesis of genetic homogeneity for Pendred's syndrome. In two sibships, mutation of the TPO gene as the cause of Pendred's syndrome could not be excluded. CONCLUSIONS: These data suggest that defects at the thyroid peroxidase locus on chromosome 2 are not the major cause of Pendred's syndrome.

14/7/7 (Item 7 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08195213 95078843
Early embryonic failure associated with uniparental disomy for human chromosome 21.
Henderson DJ; Sherman LS; Loughna SC; Bennett PR; Moore GE
Action Research Laboratory for the Molecular Biology of Fetal Development, Royal Postgraduate Medical School, Queen Charlotte's and Chelsea Hospital, London, UK.
Hum Mol Genet (ENGLAND) Aug 1994, 3 (8) p1373-6, ISSN 0964-6906
Journal Code: BRC
Languages: ENGLISH
Document type: JOURNAL ARTICLE
As many as 16% of all recognized pregnancies may be anembryonic, with failure of the embryo at a very early stage of development leaving only the extraembryonic components of the conceptus to proliferate. Studies in the mouse have shown that the maternal and paternal contributions to the genome of the zygote are not functionally equivalent, due to parental **genomic** imprinting. Uniparental disomy can reveal imprinting effects, as in this phenomenon both members of a chromosome pair are inherited from the same parent. We have carried out a systematic search for uniparental disomy in tissues from 23 cases of early embryonic failure, using **variable number tandem repeat** (VNTR) analysis and PCR amplification of polymorphic short sequence repeats. Two cases of maternal uniparental heterodisomy for chromosome 21 were identified. One case occurred in conjunction with trisomy for chromosomes 7 and 9, but in the other case maternal uniparental heterodisomy for chromosome 21 was the only chromosomal abnormality found. We therefore postulate that there may be developmentally important genes on human chromosome 21 which are imprinted such that both parental copies are essential for normal embryogenesis.

14/7/8 (Item 8 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08090783 95113701
DNA fingerprinting used to test for family effects on precocious sexual maturation in two populations of Oncorhynchus tshawytscha (Chinook salmon).
Heath DD; Iwama GK; Devlin RH
Department of Animal Science, University of British Columbia, Vancouver, Canada.
Heredity (ENGLAND) Dec 1994, 73 (Pt 6) p616-24, ISSN 0018-067X
Journal Code: G6N
Languages: ENGLISH
Document type: JOURNAL ARTICLE
Two single locus **Variable Number Tandem Repeat** (VNTR) DNA probes were used to test for differences in allele distribution between precociously mature male and immature chinook salmon, Oncorhynchus tshawytscha. Two populations were examined: Robertson Creek (RC) adult salmon, and Nicola River (NR) freshwater juveniles, or parr. **Genomic** DNA was extracted from 74 RC precociously mature adult males ('jacks') and

94 RC immature adults of the same age and from 45 NR precociously mature parr and 51 NR nonmaturing parr. The **genomic** DNA was hybridized with a single locus VNTR probe developed for chinook salmon (OtSL1), as well as one developed for Atlantic salmon, Salmo salar (Ssa1). The allele frequency distributions at both loci were significantly different for the RC jacks and immature fish, indicating a family effect on the incidence of precocious maturation in that population. No difference was found between the allele frequency distribution of the NR precocious and immature parr. A bin width sensitivity analysis showed that the comparisons of the allele frequency distributions were insensitive to the choice of bin size. No differences in heterozygosity were found between mature and immature fish at either locus for both stocks. Preliminary testing for family effects on phenotypes of interest, such as alternative life history strategies, can be performed using hypervariable VNTR DNA probes, prior to implementing costly and involved breeding programmes.

14/7/9 (Item 9 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08051141 95057304
No evidence for microsatellite instability or consistent loss of heterozygosity at selected loci in chronic myeloid leukaemia blast crisis.
Silly H; Chase A; Mills KI; Apfelbeck U; Sormann S; Goldman JM; Cross NC
LRF Centre for Adult Leukaemia, Royal Postgraduate Medical School, London, UK.
Leukemia (ENGLAND) Nov 1994, 8 (11) p1923-8, ISSN 0887-6924
Journal Code: LEU
Languages: ENGLISH
Document type: JOURNAL ARTICLE
The aim of the present study was to investigate loss of heterozygosity (LOH) or microsatellite instability in chronic myeloid leukaemia (CML) blast crisis at **genomic** locations which are known or postulated to harbour tumour suppressor genes. We studied 48 patients in blast crisis of myeloid (n = 31), lymphoid (n = 15), megakaryocytic (n = 1), or mixed lineage (n = 1) phenotype by comparing constitutional DNA extracted from buccal epithelial cells or chronic phase leucocytes with DNA obtained from blast crisis leucocytes. Twelve **variable number tandem repeat** loci from six different chromosomes were amplified by polymerase chain reaction using labelled primers, and fractionated on polyacrylamide gels. After autoradiography, length as well as intensity of the amplified products were compared between constitutional and blast crisis samples. LOH was scored as complete, partial or none in informative patients. Complete LOH was found in one patient at 8p22 and another at 13q14; partial LOH was detected in three patients at 11p13 and/or 11p15. No LOH was found at 6q27, 8p21, 18q21, 22q11-12 and 22q13 in any patient. Furthermore, no consistent difference in allelic length was observed in 517 paired amplifications indicating no microsatellite instability. We conclude that the Rb gene at 13q14, the Wilms tumour gene at 11p13, the DCC gene at 18q21, the neurofibromatosis 2 gene at 22q11-13 and uncloned tumour suppressor genes at 6q27, 8p21-22 and 11p15, as well as genes responsible for microsatellite instability, are unlikely to be involved in the progression of CML to blast crisis in the majority of patients.

14/7/10 (Item 10 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07445472 93036587
Characterization of a porcine **variable number tandem repeat** sequence specific for the glucosephosphate isomerase locus.
Davies W; Kran S; Kristensen T; Harbitz I
Department of Biochemistry, Norwegian College of Veterinary Medicine,

Oslo.
Anim Genet (ENGLAND 1992, 23 (5) p437-41, ISSN -9146
Journal Code: 4WE
Languages: ENGLISH
Document type: JOURNAL ARTICLE
A variable number of tandem repeat from a porcine glucosephosphate isomerase intron has been isolated and sequenced. The repeat has a unit size of 39 bp, is highly conserved and is present in at least 14 copies. Flanking sequences show a sequence periodicity of 53-54 bp and some sequence homology to the 39 bp repeat. A considerable part of the **genomic** DNA has been lost during subcloning and is considered to be deletion prone or refractory to propagation in E. coli. The tandem repeat is locus specific and detects at least six alleles in BamHI digested porcine DNA. No homology to other tandem repeat sequences has been found.

14/7/11 (Item 11 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07354599 91332029
Molecular cloning and analysis of the mouse homologue of the tumor-associated mucin, MUC1, reveals conservation of potential O-glycosylation sites, transmembrane, and cytoplasmic domains and a loss of minisatellite-like polymorphism.
Spicer AP; Parry G; Patton S; Gendler SJ
Molecular Epithelial Cell Biology Laboratory, Imperial Cancer Research Fund, London, United Kingdom.
J Biol Chem (UNITED STATES) Aug 15 1991, 266 (23) p15099-109, ISSN 0021-9258 Journal Code: HIV
Languages: ENGLISH
Document type: JOURNAL ARTICLE
We present here the full-length cDNA sequence and **genomic** structure of the mouse homologue of the tumor-associated mucin, MUC1. This mucin (previously called polymorphic epithelial mucin) is present at the apical surface of most glandular epithelial cells. The mouse gene, Muc-1, encodes an integral membrane protein with 40% of its coding capacity made up of serine, threonine, and proline, a composition typical of a highly O-glycosylated protein. The mucin core protein consists of an amino-terminal signal sequence, a tandem repeat domain encoding 16 repeats of 20-21 amino acids, and unique sequence containing transmembrane and cytoplasmic domains. Homology with the human protein is only 34% in the tandem repeat domain, mainly showing conservation of serines and threonines, presumed sites of O-linked carbohydrate attachment. Homology rises to 87% in the transmembrane and cytoplasmic domains, suggesting that these regions may be functionally important. The pattern of expression of the mouse mucin is very similar to that of its human counterpart and accordingly the two promoter regions share high homology, 74%, although previously identified potential hormone-responsive elements are not conserved. Interestingly, the mouse homologue, unlike its human counterpart does not exhibit a **variable number tandem repeat** polymorphism. We present evidence that suggests that the mouse gene was at one time polymorphic but has mutated away from this state.

14/7/12 (Item 12 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07344347 90368715
Molecular cloning and expression of human tumor-associated polymorphic epithelial mucin.
Gendler SJ; Lancaster CA; Taylor-Papadimitriou J; Duhig T; Peat N; Burchell J; Pemberton L; Lalani EN; Wilson D
Imperial Cancer Research Fund, Lincoln's Inn Fields, London, United

Kingdom.
J Biol Chem (UNITED STATES) Sep 5 1990, 265 p15286-93, ISSN 0021-9258 Journal Code: HIV
Languages: ENGLISH
Document type: JOURNAL ARTICLE
Human mammary cells present on the cell surface a polymorphic epithelial mucin (PEM) which is developmentally regulated and aberrantly expressed in tumors. PEM carries tumor-associated epitopes recognized by the monoclonal antibodies HMFG-1, HMFG-2, and SM-3. Previously isolated partial cDNA clones revealed that the core protein contained a large domain consisting of variable numbers of 20-amino acid repeat units. We now report the full sequence for PEM, as deduced from cDNA sequences. The encoded protein consists of three distinct regions: the amino terminus consisting of a putative signal peptide and degenerate repeats; the major portion of the protein which is the tandem repeat region; the carboxyl terminus consisting of degenerate tandem repeats and a unique sequence containing a transmembrane sequence and a cytoplasmic tail. Potential O-glycosylation sites (serines or threonines) make up more than one-fourth of the amino acids. Length variations in the tandem repeat result in PEM being an expressed **variable number tandem repeat** locus.
Tandem repeats appear to be a general characteristic of mucin core proteins.

14/7/13 (Item 13 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07245699 93145050
Automated DNA profiling by fluorescent labeling of PCR products.
Sullivan KM; Pope S; Gill P; Robertson JM
Central Research and Support Establishment, Forensic Science Service, Reading, Berks, UK.
PCR Methods Appl (UNITED STATES) Aug 1992, 2 (1) p34-40, ISSN 1054-9803 Journal Code: BNV
Languages: ENGLISH
Document type: JOURNAL ARTICLE
DNA profiling has been automated by the fluorescent tagging of amplified **variable number tandem repeat** (VNTR) loci. This was achieved by the use of fluorescently labeled primers in the amplification of 10 ng of **genomic** DNA, coupled with laser detection of the products during electrophoresis. The PCR products are sized by co-electrophoresing a standard size ladder mixed with every sample, thereby eliminating errors in size estimation caused by lane-to-lane differences in migration rate. This increases the precision of VNTR characterization and enables alleles that differ by a single 15-bp repeat to be resolved. The system is capable of high throughput: Twenty-four samples are electrophoresed and analyzed within 6 hr. Also, because four different dyes are available, three different loci can be simultaneously characterized with the fourth dye used for the internal standard. Approximately 100 unrelated British caucasians were analyzed at the loci D1S80, D17S5, and ApoB. The probabilities of two unrelated individuals matching by chance (pM) at these three loci were determined to be 0.065, 0.040, and 0.069, respectively, with a combined pM of 1.8 x 10(-4).

14/7/14 (Item 14 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06824327 92043591
Analytical DNA fingerprinting in lions: parentage; genetic diversity, and kinship.
Gilbert DA; Packer C; Pusey AE; Stephens JC; O'Brien SJ
Biological Carcinogenesis and Development Program, Program Resources,

Inc./DynCorp, NCI-Frederick Cancer Research and Development Center, Maryland 21702-1201.
J Hered (UNITED STATES) Sep-Oct 1991, 82 (5) p378-86, ISSN 0022-1503 Journal Code: IC7
Contract/Grant No.: NO1-CO-74102, CO, NCI
Languages: ENGLISH
Document type: JOURNAL ARTICLE
The application of hypervariable minisatellite **genomic** families to the reconstruction of population genetic structure holds great promise in describing the demographic history and future prospects of free-ranging populations. This potential has not yet been realized due to unforeseen empirical constraints associated with the use of heterologous species probes, to theoretical limitations on the power of the procedure to track genic heterozygosity and kinship, and to the absence of extensive field studies to test genetic predictions. We combine here the technical development of feline-specific VNTR (**variable number tandem repeat**) families of genetic loci with the long-term demographic and behavioral observations of lion populations of the Serengeti ecosystem in East Africa. Minisatellite variation was used to quantify the extent of genetic variation in several populations that differed in their natural history and levels of inbreeding. Definitive parentage, both maternal and paternal, was assessed for 78 cubs born in 11 lion prides, permitting the assessment of precise genealogical relationships among some 200 lions. The extent of DNA restriction fragment sharing between lions was empirically calibrated with the coefficient of relatedness, r, in two different populations that had distinct demographic histories. The results suggest that reliable estimates of relative genetic diversity, of parentage, and of individual relatedness can be achieved in free-ranging populations, provided the minisatellite family is calibrated in established pedigrees for the species.

14/7/15 (Item 15 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06374849 90196701
Use of multiallelic human DNA probes to detect polymorphisms in the porcine genome.
Troyer DL; Smith JE; Leipold HW
Department of Anatomy and Physiology, College of Veterinary Medicine, Kansas State University, Manhattan 66506.
Am J Vet Res (UNITED STATES) Mar 1990, 51 (3) p479-81, ISSN 0002-9645 Journal Code: 40C
Languages: ENGLISH
Document type: JOURNAL ARTICLE
Two human **variable-number tandem repeat** probes, pYNH24 and pYNA23, were examined for their possible ability to detect polymorphisms in the porcine genome. Useful DNA polymorphisms were detected in the porcine species, using both probes. In addition, results of Southern blot analysis of these markers in family studies indicated that the genome fragments obey mendelian laws of inheritance.

14/7/16 (Item 16 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

05811008 89372155
Enzymatic synthesis of DNA probes complementary to a human **variable number tandem repeat** locus.
Ali S; Wallace RB
Department of Molecular Biochemistry, Beckman Research Institute of the City of Hope, Duarte, California 91010.
Anal Biochem (UNITED STATES) Jun 1989, 179 (2) p280-3, ISSN 0003-2697

Journal Code: 4NK
Contract/Grant No.: 3672, CA, NCI
Languages: ENGLISH
Document type: JOURNAL ARTICLE

Both cloned and synthetic DNA probes complementary to human **variable number tandem repeat** (VNTR) loci have been used to detect restriction fragment length polymorphism. In this report, we describe an approach for the enzymatic synthesis of a DNA probe complementary to one VNTR locus. The probe is produced by annealing short synthetic oligonucleotides comprising single repeat units and enzymatically ligating them into a polymeric DNA probe. In HinfI digests of human **genomic** DNA separated by agarose gel electrophoresis, this ligated oligonucleotide probe (LOP) detects multiple polymorphic loci in the range of 3-23 kb producing highly informative DNA fingerprint patterns when different individuals are compared. The hybridization pattern is very stable even under high-stringency wash conditions. The LOP is more easily generated than cloned VNTR probes and is totally synthetic, avoiding problems associated with cloned probes including bacterial growth and maintenance as well as in vitro labeling.

14/7/17 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

11666796 BIOSIS NO.: 199800448527
VNTR (variable number of tandem repeat) sequences as transcriptional, translational, or functional regulators.
AUTHOR: Nakamura Yusuke(a); Koyama Kumiko; Matsushima Mieko
AUTHOR ADDRESS: (a)Lab. Mol. Med., Hum. Genome Cent., Inst. Med. Sci., Univ. Tokyo, 4-6-1 Shirokanedai, Minato-ku, **Japan
JOURNAL: Journal of Human Genetics 43 (3):p149-152 1998
ISSN: 1434-5161
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: VNTR (variable number of tandem repeat) markers, also called single-copy minisatellites, were originally isolated from human DNA as highly informative restriction fragment length polymorphisms for mapping purposes. Evidence has lately emerged that some VNTR 'sequences play significant roles in the regulation of transcription, and that some may also influence the translational efficiency or stability of mRNA, or modify the activity of proteins by altering their structure. Some apparent associations of VNTR sequences with personality traits or with susceptibility to diseases have strengthened the likelihood that these tandemly-repeated **genomic** elements are of physiological and biological importance. In this review, we summarize recent progress in efforts to clarify mechanisms involving VNTR sequences.

14/7/18 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

11521469 BIOSIS NO.: 199800302801
Genetic relationships among Japanese, Northern Han, Hui, Uygur, Kazakh, Greek, Saudi Arabian, and Italian populations based on allelic frequencies at four VNTR (D1S80, D4S43, COL2A1, D17S5) and one STR (ACTBP2) loci.
AUTHOR: Katsuyama Yoshihiko; Inoko Hidetoshi; Imanishi Tadashi; Mizuki Nobuhisa; Gojobori Takashi; Ota Masao(a)
AUTHOR ADDRESS: (a)Dep. Legal Med., Shinshu University Sch. Med., Matsumoto, Nagano**Japan
JOURNAL: Human Heredity 48 (3):p126-137 May-June, 1998

ISSN: 0001-5652
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The genetic polymorphism at four variable number of tandem repeats (D1S80, D4S43, COL2A1, D17S5) and one short tandem repeat (ACTBP2) loci was assessed by polymerase chain reaction analysis of **genomic** DNA obtained from blood samples of eight human populations (Japanese, Northern Han, Hui, Uygur, Kazakh, Saudi Arabian, Greek, Italian). Allele frequencies at all loci were in the Hardy-Weinberg equilibrium for each population. With the exception of ACTBP2, the allelic distribution patterns for these loci revealed a marked genetic divergence among the eight populations. A dendrogram constructed by the neighbor-joining method based on the allele frequencies of the five loci suggested that the five Asian populations (Japanese, Northern Han, Hui, Uygur, and Kazakh) formed one cluster, whereas the two European populations and one West Asian population (Italian, Greek, and Saudi Arabian) formed another. The genetic relationship among these populations may have been greatly influenced by admixture as a result of the migration of individuals along the Silk Road throughout history.

14/7/19 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

11006345 BIOSIS NO.: 199799627490
Usefulness of intron 40 variable number tandem repeats (VNTR) in gene tracking 14 families with type 1 and 3 von Willebrand disease.
AUTHOR: Surdhar G K; Enayat M S; Theophilus Db D M; Williams D M; Hill F G H
AUTHOR ADDRESS: Haematol. Dep., Children's Hosp. NHS Trust, Birmingham**UK
JOURNAL: British Journal of Haematology 97 (SUPPL. 1):p85 1997
CONFERENCE/MEETING: Annual Scientific Meeting of the British Society for Haematology Harrogate, England, UK April 14-17, 1997
ISSN: 0007-1048
RECORD TYPE: Citation
LANGUAGE: English

14/7/20 (Item 4 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

10753435 BIOSIS NO.: 199799374580
DNA allelic alterations within VNTR loci of scleroderma families.
AUTHOR: Artlett C M(a); Black C M; Briggs D C; Stephens C; Welsh K I
AUTHOR ADDRESS: (a)Dep. Rheumatology, Room 522 BLSB, Thomas Jefferson Univ., Philadelphia, PA 19107**USA
JOURNAL: British Journal of Rheumatology 35 (12):p1216-1222 1996
ISSN: 0263-7103
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: We have characterized genetic alterations at the molecular level in 49 scleroderma and 45 control families using variable number tandem repeats (VNTRs). Additionally, paired fibroblast cell lines from the 'affected' and 'unaffected' skin and peripheral blood leucocytes of 30 patients were also examined. All families in this study were typed for Class I Cw alleles and Class 11-DRB, -DQA and -DQB to confirm family membership. There were significant rises in the level of VNTR mutations in scleroderma patients (36.7%, n = 18), their siblings (16.3%, n = 13) and offspring (21.7%, n = 15). The level of VNTR mutations in the control group was 0.6% (n = 5). These mutations did not correlate with the

presence of autoantibodies and no patient was taking a known clastogenic drug. The most common VNTR site for mutation was pYNZ (17p13.4). Differences were also seen in the VNTR alleles between fibroblast and lymphocyte DNA from the same patient, as measured by size alteration of one of the alleles. We have found that VNTRs are unstable in scleroderma patients, relatives and offspring. The reason for the **genomic** changes remains unknown, but previous studies have implicated the presence of a clastogen.

14/7/21 (Item 5 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

09036704 BIOSIS NO.: 199497045074
Hypervariable single and multi-locus DNA polymorphisms for genetic typing of non-human primates.
AUTHOR: Wickings E Jean
AUTHOR ADDRESS: Primate Cent., CIRMF, BP 769, Franceville, Gabon**USA
JOURNAL: Primates 34 (3):p323-331 1993
ISSN: 0032-8332
DOCUMENT TYPE: Literature Review
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The series of hypervariable, "minisatellite" loci characterized by JEFFREYS and coworkers in the human myoglobin gene have proved to be DNA sequences highly conserved throughout the eukaryotic genome, and hence the methodology developed for human DNA "fingerprinting" has found immediate application in an ever expanding number of species. Primatologists have not been slow to profit from a method which predicts individual recognition to a very high degree of probability, and initial studies have focused on paternity allocation (rather than paternity exclusion, as designated by the classical biochemical markers), adaptive aspects of socio-sexual behaviour patterns and mating systems. A number of probes with sequences corresponding to the common minisatellite core sequences have been used for probing **genomic** DNA, and synthetic, G-rich oligonucleotides (15-37 bases), corresponding to the core sequence of the minisatellite repeat unit, or simply di-, tri-, or tetranucleotide repeats, appear to be equally discriminatory. The multiple banding patterns produced on hybridization of these probes to restriction enzyme digests of DNA provide an advantage in that the probability of two unrelated individuals sharing the same banding pattern will be low. However, the uncertainty of linkage of the multiple loci identified precludes genotyping and population genetic analyses based on allele frequencies. In contrast, single locus analysis allows DNA typing using **variable number tandem repeat** (VNTR) or restriction fragment length (RFLP) DNA polymorphisms, and the merits and drawbacks relative to DNA fingerprinting are discussed. For the behavioural primatologists dealing with defined, accessible troops of primates, the value of multilocus DNA fingerprinting, in terms of established methodology and availability of probes applicable to species as phylogenetically wide-ranging as apes and prosimians, may well outweigh the loss of genotypic and population structure data.

14/7/22 (Item 6 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

08947711 BIOSIS NO.: 199396099212
Parentage determination on placental tissues through deoxyribonucleic acid fingerprints.
AUTHOR: Jiang Xian-Hua(a); Wei Y
AUTHOR ADDRESS: (a)No. 2 Qishanzhong Rd., Huanggu District, Shenyang**China

JOURNAL: Annals Academy of Medicine Singapore 22 (1):p[illegible]10 1993
ISSN: 0304-4602
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Investigation of **genomic** polymorphisms detected by a mini-satellite "Myo" probe gives distinct and different Deoxyribonucleic Acid (DNA) fingerprints of chorionic villus and decidual membrane in the same placenta. The chorionic villus, which is regarded as the extraembryonal tissue, represents the essential embryonal DNA fingerprint pattern, while the decidual membrane reveals the maternal pattern. A comparison between the DNA fingerprints from the chorionic villus and from the blood sample of the suspected father provides the possibility of setting a paternity test in the early gestational state. Twenty-eight cases of paternity test on aborted placental tissues by DNA fingerprints were analysed.

14/7/23 (Item 7 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

07498879 BIOSIS NO.: 000091072748
STRUCTURE AND EXPRESSION OF THE HUMAN POLYMORPHIC EPITHELIAL MUCIN GENE AN EXPRESSED VNTR UNIT
AUTHOR: LANCASTER C A; PEAT N; DUHIG T; WILSON D; TAYLOR-PAPADIMITRIOU J; GENDLER S J
AUTHOR ADDRESS: IMPERIAL CANCER RES. FUND, P.O. BOX 123, LINCOLN'S INN FIELD, LONDON WC2A3PX, UK.
JOURNAL: BIOCHEM BIOPHYS RES COMMUN 173 (3). 1990. 1019-1029.
FULL JOURNAL NAME: Biochemical and Biophysical Research Communications
CODEN: BBRCA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: The human polymorphic epithelial mucin (PEM) is expressed apically by glandular epithelium and by the carcinomas that develop from these tissues. Previously isolated cDNA clones revealed that the core protein contained a large domain consisting of variable numbers of 60 bp tandem repeats (TR), making it an expressed minisatellite. We now report the full **genomic** sequence of the PEM gene, including 803 bp of 5'flanking sequence. The gene is composed of 7 exons and varies in size from .apprxeq.4 to .apprxeq.7 kb, depending on the number of tandem repeats in exon 2. Expression of PEM was obtained from a **genomic** clone in an Epstein-Barr virus based vector, after transfection into a human epithelial cell line, indicating the presence of effective regulatory sequences in this clone.

14/7/24 (Item 8 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

06605822 BIOSIS NO.: 000087047984
A MAPPED SET OF GENETIC MARKERS FOR HUMAN CHROMOSOME 9
AUTHOR: LATHROP M; NAKAMURA Y; O'CONNELL P; LEPPERT M; WOODWARD S; LALOUEL J-M; WHITE R
AUTHOR ADDRESS: HOWARD HUGHES MED. INST., SALT LAKE CITY, UTAH 84132.
JOURNAL: GENOMICS 3 (4). 1988. 361-366.
FULL JOURNAL NAME: Genomics
CODEN: GNMCE
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: A gentic map of markers for human chromosome 9 spanning a genetic distance of [redacted] cM in males and 231 cM in females, has been constructed from linkage studies with 19 loci in a large panel of reference families. The markers included four classical systems previously assigned to chromosome 9, and restriction fragment length polymorphisms of two cloned genes, ABL oncogene and argininosuccinase synthetase pseudogene 3 (ASSP3). The remaining 13 marker loci, with an average herterozygosity of 42%, were defined by arbitrary DNA probes newly ascertained from **genomic** libraries; seven of them were variable number of tandem repeat (VNTR) loci. A subset of 7 of the 19 linked markers is proposed for a primary map that could detect linkage with a genetic defect within the covered region of chromosome 9, provided that at least 45 phase-known meioses were available for study in an affected family.

14/7/25 (Item 1 from file: 357)
DIALOG(R)File 357:Derwent Biotechnology Abs

0201896 DBA Accession No.: 96-12667
Genetic typing by capillary electrophoresis with the allelic ladder as an absolute standard - **variable number tandem repeat** polymorphism detection
AUTHOR: Zhang N; Yeung E S
CORPORATE AFFILIATE: U.S.Dep.Environ. Univ.Iowa-State
CORPORATE SOURCE: Ames Laboratory, U.S. Department of the Environment, Ames, Iowa 50011, USA.
JOURNAL: Anal.Chem. (68, 17, 2927-31) 1996
ISSN: 0003-2700 CODEN: ANCHAM
LANGUAGE: English
ABSTRACT: A genetic typing method based on capillary electrophoresis/laser-induced fluorescence (CE-LIF) was demonstrated. **Variable number tandem repeat** polymorphisms in the human D1S80 locus were studied. A pooled allelic ladder containing the 27 most common human alleles was used as the absolute standard. Extracted **genomic** DNA from an individual was amplified by the polymerase chain reaction (PCR). Typing could be accomplished by co-injection of the PCR product and the D1S80 ladder and then running CE. Separation by a polymer solution of polyethylene oxide in uncoated fused silica capillaries allowed high-resolution, repeated runs in the same capillary. Sensitive detection with minimal sample preparation was possible by using ethidium bromide as the intercalating dye. Statistical analysis of the data showed a high level of confidence in matching the bands, despite variations in the injection process or CE system. Further adaptation to a multiple capillary array system should allow faster throughput. (20 ref)

14/7/26 (Item 2 from file: 357)
DIALOG(R)File 357:Derwent Biotechnology Abs

0148651 DBA Accession No.: 93-06703
A low profile - examination of the use of molecular biology in DNA fingerprinting forensics
AUTHOR: Salter M; Wiggins K; Keeley R H; +Jones S T; Wilson B
CORPORATE SOURCE: Metropolitan Police Forensic Science Laboratory, 109 Lambeth Road, London SE1 7LP, UK.
JOURNAL: Chem.Br. (29, 5, 419-21) 1993
CODEN: CHMBAY
LANGUAGE: English
ABSTRACT: The application of molecular biology to forensics is described. The general procedure used to produce a DNA profile is described, including (a) extraction of DNA from the sample, (b) digestion with

HinfI, (c) separation of the DNA fragments into bands by electrophoresis, [redacted] transfer of the DNA band pattern to a nylon membrane, (e) use of a 32P-labeled DNA probe to hybridize with the DNA, and (f) use of an X-ray film to reveal the positions of the bands that have hybridized with the probe. The DNA probes used have a base sequence complementary to a **variable number tandem repeat** sequence, and can be used to identify the fragments of interest from the thousands of others on the membrane. Instead of using 32P as the label, more modern techniques use alkaline phosphatase (EC-3.1.3.1) and a chemiluminescence method of detection. Further improvements can be obtained by amplification of the DNA being analyzed using the polymerase chain reaction, and adaptation of the techniques to the profiling of mitochondrial rather than **genomic** DNA. (1 ref)

14/7/27 (Item 3 from file: 357)
DIALOG(R)File 357:Derwent Biotechnology Abs

0102806 DBA Accession No.: 90-05497
Alkaline transfer of small restriction fragments from polyacrylamide gels - Southern blot hybridization of DNA after polyacrylamide gel electrophoresis; application in **variable number tandem repeat** detection
AUTHOR: Martinson J J; Clegg J B
CORPORATE SOURCE: MRC Molecular Haematology Unit, Institute of Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3 9DU, UK.
JOURNAL: Nucleic Acids Res. (18, 5, 1307) 1990
CODEN: NARHAD
LANGUAGE: English
ABSTRACT: A simple process was developed for blotting of small DNA fragments resolved by PAGE onto a cationic nylon membrane, using modified alkaline transfer. Filters could then be hybridized under standard conditions to a variety of **variable number tandem repeat** (VNTR) probes. 2.5-5.0 g **Genomic** DNA was restricted, and PAGE loading dye was added. The PAGE gel was run, and was depurinated for 20 min, while attached to a Bind-Silane-treated plate, using 0.25 M HCl. DNA was then denatured in 0.5 M NaOH for 20 min. A blotting stack was prepared, in which the alkaline solution within the gel was used as sole transfer medium, and transfer proceeded for 4 hr. The membrane was removed by soaking the glass plate, gel and membrane in water for 10 min. Gel fragments on the membrane could be rubbed off without dislodging the DNA. Pre-hybridization and hybridization to a labeled probe were then performed. Binding of the gel to 1 plate with Bind-Silane eliminated gel distortion during blot preparation. The band sharpness and resolution enabled single repeat variation to be detected with VNTR DNA probes. Resolution was achieved for 0.2-2.0 kb fragments. (8 ref)
? t s14/3,ab/28-35

14/3,AB/28 (Item 1 from file: 654)
DIALOG(R)File 654:US Pat.Full.

02987652
Utility
METHOD FOR CAPTURING A NUCLEIC ACID

PATENT NO.: 5,939,261
ISSUED: August 17, 1999 (19990817)
INVENTOR(s): Loewy, Zvi, Fair Lawn, NJ (New Jersey), US (United States of America)
Kumar, Rajan, Robbinsville, NJ (New Jersey), US (United States

of Americ[redacted]
ASSIGNEE(s): Sarnoff C[redacted]oration, (A U.S. Company or C[redacted]ration), Princeton, NJ (New Jersey), US (United States of America) [Assignee Code(s): 47766]
APPL. NO.: 8-881,282
FILED: June 24, 1997 (19970624)

This patent application is related to the following copending U.S. patent applications: Ser. No. 08-556,036, filed Nov. 9, 1995, entitled A PARTITIONED MICROELECTRONIC DEVICE ARRAY (Zanzucchi et al.); Ser. No. 08-556,423, filed Nov. 9, 1996, entitled ELECTROKINETIC PUMPING (Zanzucchi et al.); Ser. No. 08-645,966, filed May 10, 1996, entitled ELECTROKINETIC PUMPING (Zanzucchi et al.); Ser. No. 08-483,331, filed Jun. 7, 1995, entitled METHOD AND SYSTEM FOR INHIBITING CROSS-CONTAMINATION IN FLUIDS OF COMBINATORIAL CHEMISTRY DEVICE (Demers); Ser. No. 60-009,517, filed Nov. 3, 1995, which is the priority document for a regular application filed Nov. 1, 1996, and both of which are entitled ASSAY SYSTEM (Roach et al.); Ser. No. 08-745,766, filed Nov. 8, 1996, entitled FIELD-ASSISTED SEALING (Fan et al.); Ser. No. 08-786,956, filed Jan. 22, 1997, entitled PARALLEL REACTION CASSETTE AND ASSOCIATED DEVICES (Southgate et al.); Ser. No. 08-742,971, filed Nov. 1, 1996, entitled MAGNET (McBride); Ser. No. 08-554,887, filed Nov. 9, 1995, entitled METHOD OF PRODUCING MICRO-ELECTRONIC CONDUITS (Thaler et al.); Ser. No. 08-664,780, filed Jun. 14, 1996, entitled AUTOMATED NUCLEIC ACID SOLUTION (Southgate et al.); Ser. No. 08-730,636, filed Oct. 11, 1996, entitled LIQUID DISTRIBUTION SYSTEM (Demers et al.); and Ser. No. 08-838,102, filed Apr. 15, 1997, Method For Translocating Microparticles In A Microfabricated Device (Fan et al.).

This invention was made with U.S. Government support under Contract Nos. N66001-96-C-8630 and 70NANBH1037. The U.S. Government has certain rights in this invention.

FULL TEXT: 826 lines

ABSTRACT

The present invention relates to a method for capturing a class of nucleic acids comprising (a) providing a population of nucleic acids, wherein the population comprises the class; (b) binding a probe moiety to nucleic acids of the class, thereby forming one or more complexes, wherein the probe moiety is attached to a substrate; and (c) capturing the complex. The method can be implemented in certain embodiments in a structure comprised of one or more reservoirs, preferably wherein the reservoirs include one or more second chambers that are in communication with a first chamber. Preferably, the present invention is used to capture the class of nucleic acids that comprise regulatory elements included in a population of nucleic acids isolated from a cell, tissue, or organism. An alternative preferred embodiment of the present invention involves the capture of the class of nucleic acids that comprises certain repetitive elements included in a population of nucleic acids derived from an organism.

14/3,AB/29 (Item 2 from file: 654)
DIALOG(R)File 654:US Pat.Full.

02788987
Utility
COMPOSITIONS FOR CHROMOSOME-SPECIFIC STAINING
[Nucleic acid probes for in situ hybridization with labels]

PATENT NO.: 5,756,696
ISSUED: May 26, 1998 (19980526)

INVENTOR(s): Gray, Joe W., Livermore, CA (California), US (United States of America)
Pinkel, Daniel, Walnut Creek, CA (California), US (United States of America)
ASSIGNEE(s): Regents Of The University Of California, (A U.S. Company or Corporation), Oakland, CA (California), US (United States of America)
[Assignee Code(s): 13234]
APPL. NO.: 8-364,400
FILED: December 23, 1994 (19941223)

RELATED APPLICATION

This application is a continuation of U.S. Ser. No. 08-242,075, filed May 13, 1994, now abandoned, which is a continuation of U.S. Ser. No. 08-120,190, filed Sep. 13, 1993, now abandoned, which is a continuation of U.S. Ser. No. 07-862,060, filed Apr. 2, 1992, now abandoned, which is a continuation of U.S. Ser. No. 07-444,669, filed Dec. 1, 1989, now abandoned, which is a continuation in part of U.S. Ser. No. 937,793, filed Dec. 4, 1986, now abandoned which is, in turn, a continuation in part of U.S. Ser. No. 819,314, filed Jan. 16, 1986 now abandoned by the named inventors hereof and assigned to the same assignee and claims priority in said prior filed applications.

The United States Government has rights in this invention pursuant to Contract No. W-7405-ENG-48 between the U.S. Department of Energy and the University of California, for the operation of Lawrence Livermore National Laboratory.

FULL TEXT: 3373 lines

ABSTRACT

Methods and compositions for staining based upon nucleic acid sequence that employ nucleic acid probes are provided. Said methods produce staining patterns that can be tailored for specific cytogenetic analyses. Said probes are appropriate for in situ hybridization and stain both interphase and metaphase chromosomal material with reliable signals. The nucleic acid probes are typically of a complexity greater than 50 kb, the complexity depending upon the cytogenetic application. Methods are provided to disable the hybridization capacity of shared, high copy repetitive sequences and/or remove such sequences to provide for useful contrast. Still further methods are provided to produce chromosome-specific staining reagents which are made specific to the targeted chromosomal material, which can be one or more whole chromosomes, one or more regions on one or more chromosomes, subsets of chromosomes and/or the entire genome. Probes and test kits are provided for use in tumor cytogenetics, in the detection of disease related loci, in analysis of structural abnormalities, such as translocations, and for biological dosimetry. Further, methods and prenatal test kits are provided to stain targeted chromosomal material of fetal cells, including fetal cells obtained from maternal blood. Still further, the invention provides for automated means to detect and analyse chromosomal abnormalities.

02788602

Utility
SEQUENCE OF HUMAN DOPAMINE TRANSPORTER CDNA

PATENT NO.: 5,756,307
ISSUED: May 26, [illegible] (19980526)
INVENTOR(s): Uhl, George R., Towson, MD (Maryland), US (United States of America)
Vandenbergh, David, Baltimore, MD (Maryland), US (United States of America)
ASSIGNEE(s): The United States of America as represented by the Department of Health and Human Services, (A U.S. Government Agency), Washington, DC (District of Columbia, US (United States of America)
[Assignee Code(s): 6814]
APPL. NO.: 8-301,722
FILED: September 07, 1994 (19940907)

RELATED APPLICATIONS

This application is a continuation of application Ser. No. 07-889,723 filed on Jun. 1, 1992, now abandoned, which is a continuation-in-part of application Ser. No. 07-762,132 filed on Sep. 20, 1991, U.S. Pat. No. 5,312,734.

FULL TEXT: 1776 lines

ABSTRACT

The cloning and characterization of a human dopamine transporter (HUDAT) cDNA is described. RFLP analysis is used to determine the distribution of HUDAT alleles in two ethic backgrounds. The means by which the association between HUDAT alleles and behavioral disorders which have altered HUDAT expression as a basis for their etiology is discussed. Methods for evaluating the expression of HUDAT are described.

14/3,AB/31 (Item 4 from file: 654)
DIALOG(R)File 654:US Pat.Full.

02745507
Utility
VNTR PROBES AND METHODS OF USING THEREOF
[Genetic identification]

PATENT NO.: 5,716,786
ISSUED: February 10, 1998 (19980210)
INVENTOR(s): Buard, Jerome, Paris, FR (France)
Gauguier, Dominique, St Mande, FR (France)
Vergnaud, Gilles, Paris, FR (France)
ASSIGNEE(s): L'Etat Francais, represente par le Delegue Ministeriel pour l'Armement, (A Non-U.S. Goverment Entity), Armees, FR (France)
[Assignee Code(s): 7029]
APPL. NO.: 8-690,129
FILED: July 31, 1996 (19960731)
PRIORITY: 93-12923, FR (France), October 29, 1993 (19931029)

This application is a division of application Ser. No. 08-331,910, filed Oct. 31, 1994, now U.S. Pat. No. 5,573,912.

FULL TEXT: 679 lines

ABSTRACT

According to the process of the invention, sets of restriction fragments from the DNA of an individual are prepared, these restriction fragments

being separated by size. Probes are prepared by enzymatic hydrolysis of DNA from a genome bank of the species to which this individual belongs, separation of the fragments obtained as a function of their size, labeling these probes and placing them in contact, under hybridization conditions, with the aforementioned sets of restriction fragments. Finally, selection is made of the probes (capable of hybridizing with said set of restriction fragments) which do not give hybridization profiles identical to those obtained with known probes recognizing **variable number tandem repeat** regions. Applications for the probes thus obtained include, particularly, processes for identifying an individual, consanguinity testing, and investigating the origin of a seed.

14/3,AB/32 (Item 5 from file: 654)
DIALOG(R)File 654:US Pat.Full.

02724581

Utility
DETECTING GENETIC PREDISPOSITION FOR OSTEOPOROSIS
[Isolation **genomic** Dna; determination allelic pattern]

PATENT NO.: 5,698,399
ISSUED: December 16, 1997 (19971216)
INVENTOR(s): Duff, Gordon W., 18 Ashgate Road, Sheffield, S10 3BZ, S Yorks, GB (United Kingdom).England
Russell, Graham, Ronksley Farm Hollow Meadows, Sheffield, South Yorks S6 6GH, GB (United Kingdom).England
Eastell, Richard, 289 Ringinglow Road, Sheffield, S11 7PZ, GB (United Kingdom).England
[Assignee Code(s): 68000]
EXTRA INFO: Assignment transaction [Reassigned], recorded December 8, 1997 (19971208)
Assignment transaction [Reassigned], recorded July 28, 1998 (19980728)
APPL. NO.: 8-628,282
FILED: April 05, 1996 (19960405)
FULL TEXT: 632 lines

ABSTRACT

The present invention relates to methods of predicting the risk of osteoporosis. Specifically, the methods comprise isolating **genomic** DNA from an individual and determining an allelic pattern for IL-1 receptor antagonist (IL-1ra) in the **genomic** DNA. The identification of at least one copy of allele 2 indicates increased susceptibility to osteoporosis.

14/3,AB/33 (Item 6 from file: 654)
DIALOG(R)File 654:US Pat.Full.

02588755

Utility
PROCESS OF SELECTING AND/OR OBTAINING PROBES CAPABLE OF DETECTING NEW **VARIABLE NUMBER TANDEM REPEAT** REGIONS

PATENT NO.: 5,573,912
ISSUED: November 12, 1996 (19961112)
INVENTOR(s): Buard, Jerome, Paris, FR (France)
Gauguier, Dominique, St. Mande, FR (France)
Vergnaud, Gilles, Paris, FR (France)
ASSIGNEE(s): Etat Francais represente par le Deleque General pour L'Armement, (A Non-U.S. Goverment Entity), Armees, FR (France)

[Assignee Code(s): 7029]
EXTRA INFO: Assignment Transaction [Reassigned], recorded April 23, 1997 (19970423)
APPL. NO.: 8-331,910
FILED: October 31, 1994 (19941031)
PRIORITY: 93-12923, FR (France), October 29, 1993 (19931029)

FULL TEXT: 727 lines

ABSTRACT

According to the process of the invention, sets of restriction fragments from the DNA of an individual are prepared, these restriction fragments being separated by size. Probes are prepared by enzymatic hydrolysis of DNA from a genome bank of the species to which this individual belongs, separation of the fragments obtained as a function of their size, labeling these probes and placing them in contact, under hybridization conditions, with the aforementioned sets of restriction fragments. Finally, selection is made of the probes (capable of hybridizing with said set of restriction fragments) which do not give hybridization profiles identical to those obtained with known probes recognizing **variable number tandem repeat** regions. Applications for the probes thus obtained include, particularly, processes for identifying an individual, consanguinity testing, and investigating the origin of a seed.

14/3,AB/34 (Item 7 from file: 654)
DIALOG(R)File 654:US Pat.Full.

02468366

Utility
PROCESS FOR TESTING GENE-DISEASE ASSOCIATIONS

PATENT NO.: 5,464,742
ISSUED: November 07, 1995 (19951107)
INVENTOR(s): Swift, Michael R., 1004 Mt. Carmel Church Rd., Chapel Hill, NC (North Carolina), US (United States of America)
Kupper, Lawrence L., Chapel Hill, NC (North Carolina), US (United States of America)
Chase, Charles L., Chapel Hill, NC (North Carolina), US (United States of America)
ASSIGNEE(s): Swift, Michael R, (A U.S. Individual), Scarsdale, NY (New York), US (United States of America)
[Assignee Code(s): 68000]
APPL. NO.: 8-137,898
FILED: October 19, 1993 (19931019)

This application is a continuation of application Ser. No. 07-562,007, filed Aug. 2, 1990, now abandoned.

The United States Government has rights in this invention pursuant to National Institutes of Health Grants No. CA 14235 and HD 03110, awarded by the U.S. Department of Health and Human Services.

FULL TEXT: 1131 lines

ABSTRACT

The present invention describes a process to test the association of an allele and a disease, especially a non-Mendelian disease. The process involves a comparison of the proportion of test individuals who have the disease and carry the allele from a set of families in which the allele is present and the proportion of test individuals expected to carry the allele

if there is no association between the gene and the disease.

14/3,AB/35 (Item 8 from file: 654)
DIALOG(R)File 654:US Pat.Full.

02427349

Utility
REPEAT SEQUENCE CHROMOSOME SPECIFIC NUCLEIC ACID PROBES AND METHODS OF PREPARING AND USING
[Primer directed DNA amplification using degenerate primers to isolate efficiently chromosome-specific repeated DNA]

PATENT NO.: 5,427,932
ISSUED: June 27, 1995 (19950627)
INVENTOR(s): Weier, Heinz-Ulrich G., Tracy, CA (California), US (United States of America)
Gray, Joe W., San Francisco, CA (California), US (United States of America)
ASSIGNEE(s): Reagents of the University of California, (A U.S. Company or Corporation), Oakland, CA (California), US (United States of America)
[Assignee Code(s): 13234]
APPL. NO.: 7-858,124
FILED: March 26, 1992 (19920326)

RELATED APPLICATIONS

This application is a continuation-in-part application of U.S. Ser. No. 07-683,441 filed Apr. 9, 1991, now abandoned. Priority in said prior filed applications is herein claimed.

The United States Government has rights in this invention pursuant to Contract No. W-7405-ENG-48 between the United States Department of Energy and the University of California for the operation of Lawrence Livermore National Laboratory.

FULL TEXT: 2094 lines

ABSTRACT

A primer directed DNA amplification method to isolate efficiently chromosome-specific repeated DNA wherein degenerate oligonucleotide primers are used is disclosed. The probes produced are a heterogeneous mixture that can be used with blocking DNA as a chromosome-specific staining reagent, and/or the elements of the mixture can be screened for high specificity, size and/or high degree of repetition among other parameters. The degenerate primers are sets of primers that vary in sequence but are substantially complementary to highly repeated nucleic acid sequences, preferably clustered within the template DNA, for example, pericentromeric alpha satellite repeat sequences. The template DNA is preferably chromosome-specific. Exemplary primers ard probes are disclosed. The probes of this invention can be used to determine the number of chromosomes of a specific type in metaphase spreads, in germ line and/or somatic cell interphase nuclei, micronuclei and/or in tissue sections. Also provided is a method to select arbitrarily repeat sequence probes that can be screened for chromosome-specificity.
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***Newweek Flltext (File 482)
***WIPO/PCT Patent Flltext (File 349)

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File   1:ERIC  1966-2000/Feb
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File 410:Chronolog(R)  1981-2000 Mar/Apr
       (c) 2000 The Dialog Corporation plc

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            25  FRAGMENT
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? b 155, 5, 399, 357, 654

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*File 155: MEDLINE will be reloaded. Accession numbers will change.
  File   5:Biosis Previews(R)  1969-2000/Apr W3
        (c) 2000 BIOSIS
  File 399:CA SEARCH(R)  1967-2000/UD=13216
        (c) 2000 American Chemical Society
*File 399: Use is subject to the terms of your user/customer agreement.
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  File 357:Derwent Biotechnology Abs  1982-2000/Apr B2
        (c) 2000 Derwent Publ Ltd
  File 654:US Pat.Full  1990-2000/Apr 11
        (c) format only 2000 The Dialog Corp.
*File 654: Reassignment data current through 12/06/1999 recordings.
Due to recent processing problems, the SORT command is not working.

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? s genomic and tag and fragment and oligonucleotide

         130463  GENOMIC
          29747  TAG
         256010  FRAGMENT
          82918  OLIGONUCLEOTIDE
      S1   2820  GENOMIC AND TAG AND FRAGMENT AND OLIGONUCLEOTIDE
? s s1 and polymorphism

           2820  S1
         160329  POLYMORPHISM
      S2    464  S1 AND POLYMORPHISM
? s s2 and (VNTR or (variable(w)number(w)tandem(w)repeat))

            464  S2
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         54940  TANDEM
        135318  REPEAT
           461  VARIABLE(W)NUMBER(W)TANDEM(W)REPEAT
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? t s4/6/1-20


 4/6/1     (Item 1 from file: 654)
03084775
METHODS OF DETECTING ALZHEIMER'S DISEASE
FULL TEXT:        1496 lines


 4/6/2     (Item 2 from file: 654)
03084769
METHODS AND COMPOSITIONS FOR ENHANCING SENSITIVITY IN THE ANALYSIS OF
BIOLOGICAL-BASED ASSAYS
FULL TEXT:        5884 lines


 4/6/3     (Item 3 from file: 654)
03067992
DNA BRACKETING LOCUS COMPATIBLE STANDARDS FOR ELECTROPHORESIS
FULL TEXT:        1867 lines


 4/6/4     (Item 4 from file: 654)
02983945
DETECTION OF HYPERMUTABLE NUCLEIC ACID SEQUENCE IN TISSUE
FULL TEXT:        1815 lines


 4/6/5     (Item 5 from file: 654)
02893131
METHOD OF CHARACTERISATION OF GENOMIC DNA
FULL TEXT:        4623 lines


 4/6/6     (Item 6 from file: 654)
02893130
DIAGNOSIS OF RETINOBLASTOMA
FULL TEXT:        1223 lines


 4/6/7     (Item 7 from file: 654)
02881547
MULTIPLEX AMPLIFICATION OF SHORT TANDEM REPEAT LOCI
FULL TEXT:        3051 lines


 4/6/8     (Item 8 from file: 654)
02871149
GENE SEQUENCE FOR SPINOCEREBELLAR ATAXIA TYPE 1 AND METHOD FOR DIAGNOSIS
[For diagnosis of autosomal dominant spinocerebellar ataxia type 1 gene]
FULL TEXT:        4786 lines
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4/6/9 (Item 9 from file: 654)
02846423
METHOD OF CHARACTERISATION
[Amplification of tandemly repeated region of **genomic** DNA, separation of set of amplification products to provide sample code]
FULL TEXT: 3543 lines

4/6/10 (Item 10 from file: 654)
02846421
COMPOSITIONS AND USES THEREOF IN THE DIAGNOSIS OF PSORIASIS
[Screening for psoriasis susceptibility by determining in a nucleic acid sample the presence of a polymorphic marker linked with a gene for interleukin enhancer binding factor]
FULL TEXT: 2235 lines

4/6/11 (Item 11 from file: 654)
02816905
APC (ADENOMATOUS POLYOSIS COLI) PROTEIN
[Hybrid]
FULL TEXT: 3924 lines

4/6/12 (Item 12 from file: 654)
02816663
ALLELIC LADDERS FOR SHORT TANDEM REPEAT LOCI
[Detecting Dna sequernces]
FULL TEXT: 1268 lines

4/6/13 (Item 13 from file: 654)
02716697
APC ANTIBODIES
FULL TEXT: 4328 lines

4/6/14 (Item 14 from file: 654)
02698037
ALLELIC LADDERS FOR SHORT TANDEM REPEAT LOCI
[Detection of alleles by comparing three polymerase chain reaction co-amplified short tandem DNA repeat sequences with allelic ladder]
FULL TEXT: 1262 lines

4/6/15 (Item 15 from file: 654)
02668237
DETECTION OF INHERITED AND SOMATIC MUTATIONS OF APC GENE IN COLORECTAL CANCER OF HUMANS
FULL TEXT: 4452 lines

4/6/16 (Item 16 from file: 654)
02616589
ALLELIC LADDERS FOR SHORT TANDEM REPEAT LOCI
[Markers for detection of specific DNA sequences, also kits]
FULL TEXT: 1261 lines

4/6/17 (Item 17 from file: 654)
02451514
CHROMOSOME 14 AND FAMILIAL ALZHEIMERS DISEASE GENETIC MARKERS AND ASSAYS
FULL TEXT: 3467 lines

4/6/18 (Item 18 from file: 654)
02409494
GENETIC IDENTIFICATION EMPLOYING DNA PROBES OF **VARIABLE NUMBER TANDEM REPEAT** LOCI
FULL TEXT: 2125 lines

4/6/19 (Item 19 from file: 654)
02357021
DNA TYPING WITH SHORT TANDEM REPEAT POLYMORPHISMS AND IDENTIFICATION OF POLYMORPHIC SHORT TANDEM REPEATS
FULL TEXT: 1738 lines

4/6/20 (Item 20 from file: 654)
01913496
GENETIC IDENTIFICATION EMPLOYING DNA PROBES OF **VARIABLE NUMBER TANDEM REPEAT** LOCI
[IDENTIFICATION OF CLONED DNA SEQUENCES]
FULL TEXT: 2145 lines
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Set	Items	Description
S1	2820	GENOMIC AND TAG AND FRAGMENT AND OLIGONUCLEOTIDE
S2	464	S1 AND POLYMORPHISM
S3	20	S2 AND (VNTR OR (VARIABLE(W)NUMBER(W)TANDEM(W)REPEAT))
S4	20	RD (unique items)

? t s4/3,ab/5,7,9,14-20

4/3,AB/5 (Item 5 from file: 654)
DIALOG(R)File 654:US Pat.Full.

02893131
Utility
METHOD OF CHARACTERISATION OF **GENOMIC** DNA

PATENT NO.: 5,853,989
ISSUED: December 29, 1998 (19981229)
INVENTOR(s): Jeffreys, Alec John, Leicester, GB (United Kingdom).Great Britian
Little, Stephen, Chester, GB (United Kingdom).Great Britian
Ferrie, Richard Mark, Cheshire, GB (United Kingdom).Great Britian
Brownie, Jannine, Cheshire, GB (United Kingdom).Great Britian
ASSIGNEE(s): Zeneca Limited, (A Non-U.S. Company or Corporation), London, GB (United Kingdom)
[Assignee Code(s): 32757]
APPL. NO.: 8-643,181
FILED: May 06, 1996 (19960506)
PRIORITY: 9118371, GB (United Kingdom), August 27, 1991 (19910827)
9119089, GB (United Kingdom), September 6, 1991 (19910906)
9124636, GB (United Kingdom), November 20, 1991 (19911120)
9207379, GB (United Kingdom), April 3, 1992 (19920403)
9212627, GB (United Kingdom), June 15, 1992 (19920615)
9212881, GB (United Kingdom), June 17, 1992 (19920617)

This application is a continuation-in-part of application of Ser. No. 08-418,859 filed Apr. 5, 1995 which is a continuation of 07-935,107, filed Aug. 26, 1992 now abandoned.

FULL TEXT: 4623 lines

ABSTRACT

The present invention relates generally to a method of characterizing a sample of **genomic** DNA and to nucleotide sequences employed in the method as well as kits comprising these. In particular the invention involves the use of primers which selectively prime specific type(s) of internal repeat unit in a tandemly repeated region. The method of the invention is particularly useful in forensic or paternity studies and provides individual sample codes suitable for computerized storage on, and retrieval from, a database.

4/3,AB/7 (Item 7 from file: 654)
DIALOG(R)File 654:US Pat.Full.

02881547

Utility
MULTIPLEX AMPLIFICATION OF SHORT TANDEM REPEAT LOCI

PATENT NO.: 5,843,660
ISSUED: December 01, 1998 (19981201)
INVENTOR(s): Schumm, James W., Madison, WI (Wisconsin), US (United States of America)
Micka, Katherine A., Oregon, WI (Wisconsin), US (United States of America)
Rabbach, Dawn R., DeForest, WI (Wisconsin), US (United States of America)
ASSIGNEE(s): Promega Corporation, (A U.S. Company or Corporation), Madison, WI (Wisconsin), US (United States of America)
[Assignee Code(s): 18871]
APPL. NO.: 8-632,575
FILED: April 15, 1996 (19960415)

This application is a continuation-in-part of U.S. patent application Ser. No. 08-316,544, filed Sep. 30, 1994. The entire disclosure of that parent application is incorporated by reference herein.

FULL TEXT: 3051 lines

ABSTRACT

The present invention is directed to the simultaneous amplification of multiple distinct genetic loci using PCR or other amplification systems to determine in one reaction the alleles of each of the loci contained within the multiplex.

4/3,AB/9 (Item 9 from file: 654)
DIALOG(R)File 654:US Pat.Full.

02846423

Utility
METHOD OF CHARACTERISATION
[Amplification of tandemly repeated region of **genomic** DNA, separation of set of amplification products to provide sample code]

PATENT NO.: 5,811,235
ISSUED: September 22, 1998 (19980922)

INVENTOR(s): Jeffreys, Alec John, Leicester, GB (United Kingdom).England
ASSIGNEE(s): Zeneca Limited, (A Non-U.S. Company or Corporation), London, GB (United Kingdom) England
[Assignee Code(s): 32757]
APPL. NO.: 8-418,859
FILED: April 05, 1995 (19950405)
PRIORITY: 9118371, GB (United Kingdom), August 27, 1991 (19910827)
9119089, GB (United Kingdom), September 6, 1991 (19910906)
9124636, GB (United Kingdom), November 20, 1991 (19911120)
9207379, GB (United Kingdom), April 3, 1992 (19920403)
9212627, GB (United Kingdom), June 15, 1992 (19920615)
9212881, GB (United Kingdom), June 17, 1992 (19920617)

This is a continuation of application Ser. No. 07-935,107, filed Aug. 26, 1992, now abandoned.

FULL TEXT: 3543 lines

ABSTRACT

A method of characterizing a test sample of **genomic** DNA which method comprises amplifying a tandemly repeated region, comprising more than one type of repeat unit, as far as internal repeat units of a specific type so as to generate a set of amplification products which identify the relative positions of the internal repeat units within the tandemly repeated region, and separating the set of amplification products to provide a sample code. The sample codes are suitable for computerized storage on, and retrieval from, a database. The invention also provides a novel method for the detection of diagnostic base sequences in one or more nucleic acids contained in a sample.

4/3,AB/14 (Item 14 from file: 654)
DIALOG(R)File 654:US Pat.Full.

02698037
Utility
ALLELIC LADDERS FOR SHORT TANDEM REPEAT LOCI
[Detection of alleles by comparing three polymerase chain reaction co-amplified short tandem DNA repeat sequences with allelic ladder]

PATENT NO.: 5,674,686
ISSUED: October 07, 1997 (19971007)
INVENTOR(s): Schumm, James W., Madison, WI (Wisconsin), US (United States of America)
Puers, Christoph, Madison, WI (Wisconsin), US (United States of America)
ASSIGNEE(s): Promega Corporation, (A U.S. Company or Corporation), Madison, WI (Wisconsin), US (United States of America)
[Assignee Code(s): 18871]
EXTRA INFO: Assignment transaction [Reassigned], recorded October 13, 1998 (19981013)
APPL. NO.: 8-515,236
FILED: August 15, 1995 (19950815)

This is a divisional of application Ser. No. 08-219,633, filed Mar. 28, 1994.

FULL TEXT: 1262 lines

ABSTRACT

The present invention is directed to an assay system and kit and a process for detecting at least one short tandem repeat sequence from DNA at a specific locus utilizing an allelic ladder containing at least two short tandem repeat sequences of the same lengths as two or more known alleles for the locus.

4/3,AB/15 (Item 15 from file: 654)
DIALOG(R)File 654:US Pat.Full.

02668237

Utility
DETECTION OF INHERITED AND SOMATIC MUTATIONS OF APC GENE IN COLORECTAL CANCER OF HUMANS

PATENT NO.: 5,648,212
ISSUED: July 15, 1997 (19970715)
INVENTOR(s): Albertsen, Hans, Salt Lake City, UT (Utah), US (United States of America)
Anand, Rakesh, Cheshire, GB (United Kingdom).England
Carlson, Mary, Salt Lake City, UT (Utah), US (United States of America)
Groden, Joanna, Salt Lake City, UT (Utah), US (United States of America)
Hedge, Philip John, Cheshire, GB (United Kingdom).England
Joslyn, Geoff, Salt Lake City, UT (Utah), US (United States of America)
Kinzler, Kenneth, Baltimore, MD (Maryland), US (United States of America)
Markham, Alexander, Cheshire, GB (United Kingdom).England
Nakamura, Yusuke, Tokyo, JP (Japan)
Thliveris, Andrew, Salt Lake City, UT (Utah), US (United States of America)
Vogelstein, Bert, Baltimore, MD (Maryland), US (United States of America)
White, Raymond L., Salt Lake City, UT (Utah), US (United States of America)
ASSIGNEE(s): Japanese Foundation for Cancer Research Cancer Institute, (A Non-U.S. Company or Corporation), Tokyo, JP (Japan)
The John Hopkins University, (A U.S. Company or Corporation), Baltimore, MD (Maryland), US (United States of America)
University of Utah, (A U.S. Company or Corporation), Salt Lake City, UT (Utah), US (United States of America)
Zeneca Limited, (A Non-U.S. Company or Corporation), Cheshire, GB (United Kingdom) England
[Assignee Code(s): 12629; 32757; 39884; 88042]
APPL. NO.: 8-289,548
FILED: August 12, 1994 (19940812)
PRIORITY: 9100962, GB (United Kingdom), January 16, 1991 (19910116)
9100963, GB (United Kingdom), January 16, 1991 (19910116)
9100974, GB (United Kingdom), January 16, 1991 (19910116)
9100975, GB (United Kingdom), January 16, 1991 (19910116)
This application is a division of application Ser. No. 07-741,940, filed Aug. 8, 1991, which issued as U.S. Pat. No. 5,352,775.

FULL TEXT: 4452 lines

ABSTRACT

Methods are provided for assessing mutations of the APC gene in human tissues and body samples. APC mutations are found in familial adenomatous polyposis patients as well as in sporadic colorectal cancer patients. APC is expressed in most normal tissues. APC is a tumor suppressor.

4/3,AB/16 (Item 16 from file: 654)
DIALOG(R)File 654:US Pat.Full.

02616589

Utility
ALLELIC LADDERS FOR SHORT TANDEM REPEAT LOCI
[Markers for detection of specific DNA sequences, also kits]

PATENT NO.: 5,599,666
ISSUED: February 04, 1997 (19970204)
INVENTOR(s): Schumm, James W., Madison, WI (Wisconsin), US (United States of America)
Puers, Christoph, Madison, WI (Wisconsin), US (United States of America)
ASSIGNEE(s): Promega Corporation, (A U.S. Company or Corporation), Madison, WI (Wisconsin), US (United States of America)
[Assignee Code(s): 18871]
APPL. NO.: 8-219,633
FILED: March 28, 1994 (19940328)

FULL TEXT: 1261 lines

ABSTRACT

The present invention is directed to an assay system, a kit and a process for detecting at least one short tandem repeat sequence from DNA at a specific locus utilizing an allelic ladder containing at least two short tandem repeat sequences of the same lengths as two or more known alleles for the locus.

4/3,AB/17 (Item 17 from file: 654)
DIALOG(R)File 654:US Pat.Full.

02451514

Utility
CHROMOSOME 14 AND FAMILIAL ALZHEIMERS DISEASE GENETIC MARKERS AND ASSAYS

PATENT NO.: 5,449,604
ISSUED: September 12, 1995 (19950912)
INVENTOR(s): Schellenberg, Gerard D., Seattle, WA (Washington), US (United States of America)
Bird, Thomas D., Seattle, WA (Washington), US (United States of America)
Wijsman, Ellen M., Seattle, WA (Washington), US (United States of America)
ASSIGNEE(s): University of Washington, (A U.S. Company or Corporation), Seattle, WA (Washington), US (United States of America)
[Assignee Code(s): 2937]
APPL. NO.: 7-964,151
FILED: October 21, 1992 (19921021)

This invention was made with government support under grant AG08017 awarded by the National Institute on Aging and grant R01MH43240 awarded by

the National Institute of Mental Health. The government has certain rights in the invention.

FULL TEXT: 3467 lines

ABSTRACT

Method for isolating a DNA segment indicative of an Alzheimer's disease trait in a family population, wherein said family population consists essentially of a plurality of blood relatives of an individual having a chromosome 14 Alzheimer's disease trait, by: preparing a test sample of immobilized separated **genomic** DNA fragments from a plurality of the blood relatives, contacting each of the test samples with a test **oligonucleotide** under conditions permitting hybridization of complementary single stranded DNA molecules, wherein the test **oligonucleotide** is complementary with at least a portion of a genetic marker located between band q11.2 and band q32.1 in chromosome 14, identifying a plurality of hybridized molecules so formed as alleles of the genetic marker in the family population, identifying one of the genetic marker alleles as indicative of the Alzheimer's disease trait in the family population by either determining by pedigree analysis a segregation value for each of the genetic markers alleles and the Alzheimer's disease trait, and selecting an indicative genetic marker allele that co-segregates with the Alzheimer's disease trait in the family population, or measuring genetic linkage between each of the genetic marker alleles and the Alzheimer's disease trait, and selecting a genetic marker allele as indicative of the Alzheimer's disease trait in the family population if the selected genetic marker allele has a maximal LOD score of at least 3 at a recombination fraction of about 0.0 to about 0.1 for genetic linkage with the Alzheimer's disease trait in the family population, and isolating a chromosome 14 DNA segment containing the indicative genetic marker allele.

4/3,AB/18 (Item 18 from file: 654)
DIALOG(R)File 654:US Pat.Full.

02409494

Utility

GENETIC IDENTIFICATION EMPLOYING DNA PROBES OF **VARIABLE NUMBER TANDEM REPEAT** LOCI

PATENT NO.: 5,411,859
ISSUED: May 02, 1995 (19950502)

INVENTOR(s): White, Raymond L., Salt Lake City, UT (Utah), US (United States of America)
Nakamura, Yusuke, Salt Lake City, UT (Utah), US (United States of America)
O'Connell, Peter, Salt Lake City, UT (Utah), US (United States of America)
Midvale, Salt Lake City, UT (Utah), US (United States of America)
Leppert, Mark F., Salt Lake City, UT (Utah), US (United States of America)
ASSIGNEE(s): University of Utah Research Foundation, (A U.S. Company or Corporation), Salt Lake City, UT (Utah), US (United States of America)
[Assignee Code(s): 88042]

EXTRA INFO: Assignment transaction [Reassigned], recorded April 29, 1998 (19980429)
Assignment transaction [Reassigned], recorded February 26, 1999 (19990226)
APPL. NO.: 7-728,751
FILED: June 10, 1991 (19910610)

CROSS REFERENCE TO RELATED APPLICATIONS

This application is a continuation of application Ser. No. 07-597,039, filed Oct. 15, 1990, now abandoned, which is divisional of application Ser. No. 07-307,820, filed Feb. 8, 1989, now U.S. Pat. No. 4,963,663, which is a continuation-in-part of application Ser. No. 07-288,835, filed Dec. 23, 1988, now abandoned, which is a continuation-in-part of application Ser. No. 07-282,141, filed Dec. 9, 1988, now abandoned, which is a continuation-in-part of application Ser. No. 07-157,962, filed Feb. 18, 1988, now abandoned.

FULL TEXT: 2125 lines

ABSTRACT

The present invention is related to the identification of cloned DNA sequences that reveal individual multiallele loci. The loci are used in the process of the present invention to provide convenient and accurate genetic identification. A large number of clones that recognize **VNTR** loci have been isolated from a cosmid library and characterized.

4/3,AB/19 (Item 19 from file: 654)
DIALOG(R)File 654:US Pat.Full.

02357021

Utility

DNA TYPING WITH SHORT TANDEM REPEAT POLYMORPHISMS AND IDENTIFICATION OF POLYMORPHIC SHORT TANDEM REPEATS

PATENT NO.: 5,364,759
ISSUED: November 15, 1994 (19941115)

INVENTOR(s): Caskey, Charles T., Houston, TX (Texas), US (United States of America)
Edwards, Albert O., Houston, TX (Texas), US (United States of America)
ASSIGNEE(s): Baylor College of Medicine, (A U.S. Company or Corporation), Houston, TX (Texas), US (United States of America)
[Assignee Code(s): 6345]

EXTRA INFO: Reexamined, certified November 18, 1997 (19971118)
Reexamined, certified July 20, 1999 (19990720)
APPL. NO.: 7-647,655
FILED: January 31, 1991 (19910131)

FULL TEXT: 1738 lines

ABSTRACT

The present invention relates to a DNA profiling assay for detecting polymorphisms in a short tandem repeat. The method includes the steps of extracting DNA from a sample to be tested, amplifying the extracted DNA and identifying the amplified extension products for each different sequence. Each different sequence is differentially labeled. In the method, internal and external standards can also be used. The method is applicable to a wide variety of forensic and medical samples, including blood, semen, vaginal swaps, tissue, hair, saliva, urine and mixtures of body fluids. A short tandem repeat sequence which can be characterized by the formula (A sub w G sub x T sub y C sub z) sub n, wherein A, G, T and C represent the nucleotides, w, x, y and z represent the number of nucleotide and range from 0 to 7 and the sum of w+x+y+z ranges from 3 to 7 and n represents the repeat number and ranges from 5 to 50. The labels can be from a variety of groups, including fluorescers, radioisotopes, chemiluminescers, stains, enzymes and antibodies. Also described is a kit. Further, a method of

detecting the polymorphic short tandem repeats comprising the steps of either searching for the repeats in a database or comparing oligonucleotides and searching for the repeats in a genetic library.

4/3,AB/20 (Item 20 from file: 654)
DIALOG(R)File 654:US Pat.Full.

01913496

Utility
GENETIC IDENTIFICATION EMPLOYING DNA PROBES OF **VARIABLE NUMBER TANDEM REPEAT** LOCI
[IDENTIFICATION OF CLONED DNA SEQUENCES]

PATENT NO.: 4,963,663
ISSUED: October 16, 1990 (19901016)
INVENTOR(s): White, Raymond L., Salt Lake City, UT (Utah), US (United States of America)
Nakamura, Yusuke, Salt Lake City, UT (Utah), US (United States of America)
O'Connell, Peter, Midvale, UT (Utah), US (United States of America)
Leppert, Mark F., Salt Lake City, UT (Utah), US (United States of America)
ASSIGNEE(s): University of Utah, (A U.S. Company or Corporation), Salt Lake City, UT (Utah), US (United States of America)
[Assignee Code(s): 88042]
EXTRA INFO: Assignment transaction [Reassigned], recorded March 3, 1992 (19920303)
Assignment transaction [Reassigned], recorded April 29, 1998 (19980429)
Assignment transaction [Reassigned], recorded February 26, 1999 (19990226)
APPL. NO.: 7-307,820
FILED: February 08, 1989 (19890208)

CROSS REFERENCE TO RELATED APPLICATION

This application is a continuation-in-part of application Ser. No. 288,835, filed Dec. 23, 1988 which is a continuation-in-part of application Ser. No. 282,141, filed Dec. 9, 1988 which is a continuation-in-part of application Ser. No. 157,962 filed Feb. 18, 1988.

FULL TEXT: 2145 lines

ABSTRACT

The present invention is related to the identification of cloned DNA sequences that reveal individual multiallele loci. The loci are used in the process of the present invention to provide convenient and accurate genetic identification. A large number of clones that recognize **VNTR** loci have been isolated from a cosmid library and characterized.
? ds

Set	Items	Description
S1	2820	GENOMIC AND TAG AND FRAGMENT AND OLIGONUCLEOTIDE
S2	464	S1 AND POLYMORPHISM
S3	20	S2 AND (VNTR OR (VARIABLE(W)NUMBER(W)TANDEM(W)REPEAT))
S4	20	RD (unique items)

? rd s2

>>>Duplicate detection is not supported for File 654.

>>>Records from unsupported files will be retained in RD set.
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...examined 50 records (100)
...examined 50 records (150)
...examined 50 records (200)
...examined 50 records (250)
...examined 50 records (300)
...examined 50 records (350)
...examined 50 records (400)
...examined 50 records (450)
...completed examining records
Processing
S5 464 RD S2 (unique items)
? t s5/6/1-20

5/6/1 (Item 1 from file: 654)
03107586
HUMAN T CELL REACTIVE FELINE PROTEIN (TRFP) ISOLATED FROM HOUSE DUST AND USES THEREFOR
FULL TEXT: 5293 lines

5/6/2 (Item 2 from file: 654)
03107462
OB POLYPEPTIDES AS MODULATORS OF BODY WEIGHT
FULL TEXT: 7560 lines

5/6/3 (Item 3 from file: 654)
03107334
COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
FULL TEXT: 5804 lines

5/6/4 (Item 4 from file: 654)
03107314
METHOD FOR IDENTIFYING VARIATIONS IN POLYNUCLEOTIDE SEQUENCES
FULL TEXT: 4156 lines

5/6/5 (Item 5 from file: 654)
03104538
ISOLATED TRBP POLYPEPTIDES AND USES THEREFOR
FULL TEXT: 4296 lines

5/6/6 (Item 6 from file: 654)
03104388
UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES THEREOF
FULL TEXT: 6726 lines

5/6/7 (Item 7 from file: 654)
03104262
ARF-P19, A NOVEL REGULATOR OF THE MAMMALIAN CELL CYCLE
FULL TEXT: 4924 lines

5/6/8 (Item 8 from file: 654)
03104258
POLYNUCLEOTIDES ENCODING INSULIN HOMOLOG ZINS3

FULL TEXT: 2195 lines

5/6/9 (Item 9 from file: 654)
03104239
DIAGNOSIS AND TREATMENT OF GLAUCOMA
FULL TEXT: 1271 lines

5/6/10 (Item 10 from file: 654)
03104227
MATERIALS AND METHODS RELATING TO THE IDENTIFICATION AND SEQUENCING OF THE BRCA2 CANCER SUSCEPTIBILITY GENE AND USES THEREOF
FULL TEXT: 9257 lines

5/6/11 (Item 11 from file: 654)
03104034
METHOD FOR DETECTING B. BURGDORFERI INFECTION
FULL TEXT: 951 lines

5/6/12 (Item 12 from file: 654)
03104024
PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE
FULL TEXT: 4757 lines

5/6/13 (Item 13 from file: 654)
03101292
EPSTEIN BARR VIRUS INDUCED GENES
FULL TEXT: 2093 lines

5/6/14 (Item 14 from file: 654)
03101287
COMPOSITIONS FOR THE TREATMENT AND DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
FULL TEXT: 4382 lines

5/6/15 (Item 15 from file: 654)
03101030
PROSTATE/COLON TUMOR SUPPRESSOR GENE LOCATED ON HUMAN CHROMOSOME 8
FULL TEXT: 3676 lines

5/6/16 (Item 16 from file: 654)
03100997
MAMMALIAN PRO-APOPTOTIC BOK GENES AND THEIR USES
FULL TEXT: 1936 lines

5/6/17 (Item 17 from file: 654)
03100982
CSAK-3 NUCLEIC ACID MOLECULES AND USES THEREFOR
FULL TEXT: 5198 lines

5/6/18 (Item 18 from file: 654)
03097788
VASCULAR ENDOTHELIAL GROWTH FACTOR 2
FULL TEXT: 5072 lines

5/6/19 (Item 19 from file: 654)
03094632
ISOLATED NUCLEIC ACID ENCODING TRBP
FULL TEXT: 4285 lines

5/6/20 (Item 20 from file: 654)
03094618
POLYPEPTIDE OF N-ACETYLGLUCOSAMINE-6-O-SULFOTRANSFERASE AND DNA ENCODING THE SAME
FULL TEXT: 1985 lines
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$0.57 Estimated cost File155
$1.11 0.198 DialUnits File5
$1.11 Estimated cost File5
$2.25 0.179 DialUnits File399
$2.25 Estimated cost File399
$1.02 0.087 DialUnits File357
$1.02 Estimated cost File357
$7.72 1.309 DialUnits File654
$0.00 40 Type(s) in Format 6
$9.50 10 Type(s) in Format 4 (UDF)
$9.50 50 Types
$17.22 Estimated cost File654
OneSearch, 5 files, 1.952 DialUnits FileOS
$0.30 TYMNET
$22.47 Estimated cost this search
$23.03 Estimated total session cost 2.156 DialUnits
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